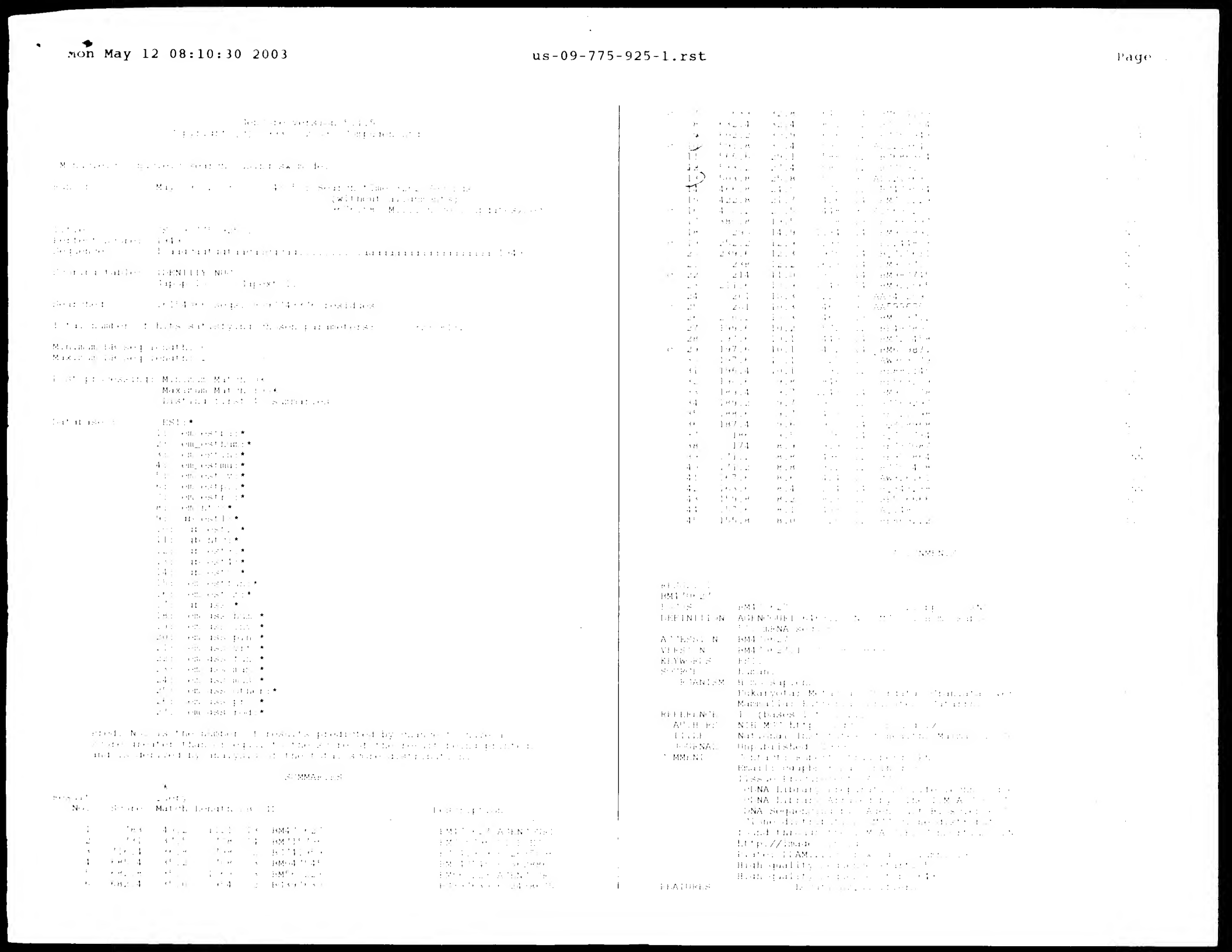


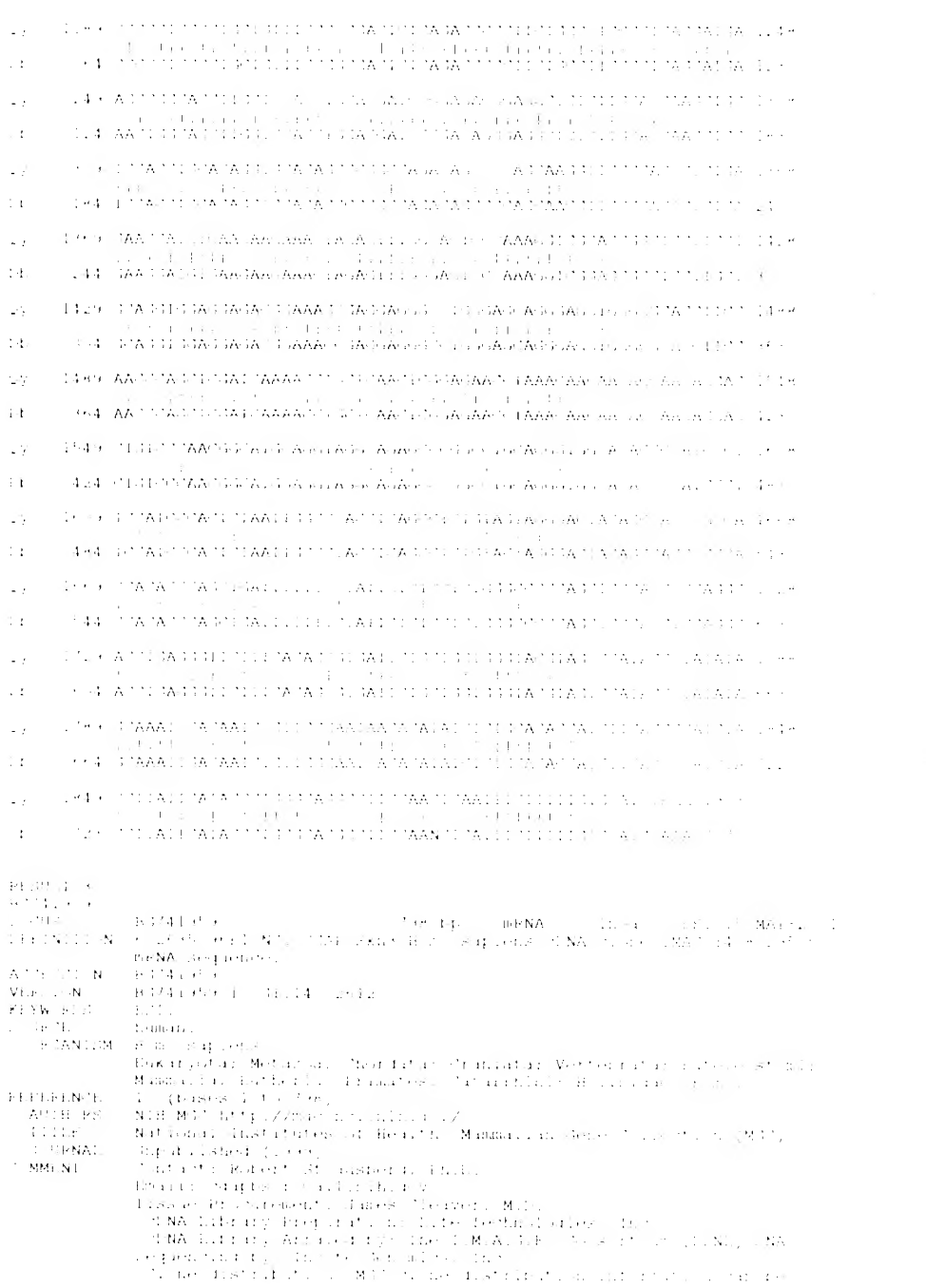
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:753442"
/clone_lib="NIH_MGC_71"
/tissue_type="teratocarcinoma"
/lab_host="DH10B (phage resistant)"
/note="vector: pCMV-SPORT6; Vector pCMV-SPORT6 was used to construct this library. Not I
Site 2; Sall; treated unidirectional; Size=1.5-4.8 kb; Insert
Average insert size 2.1 kb; "

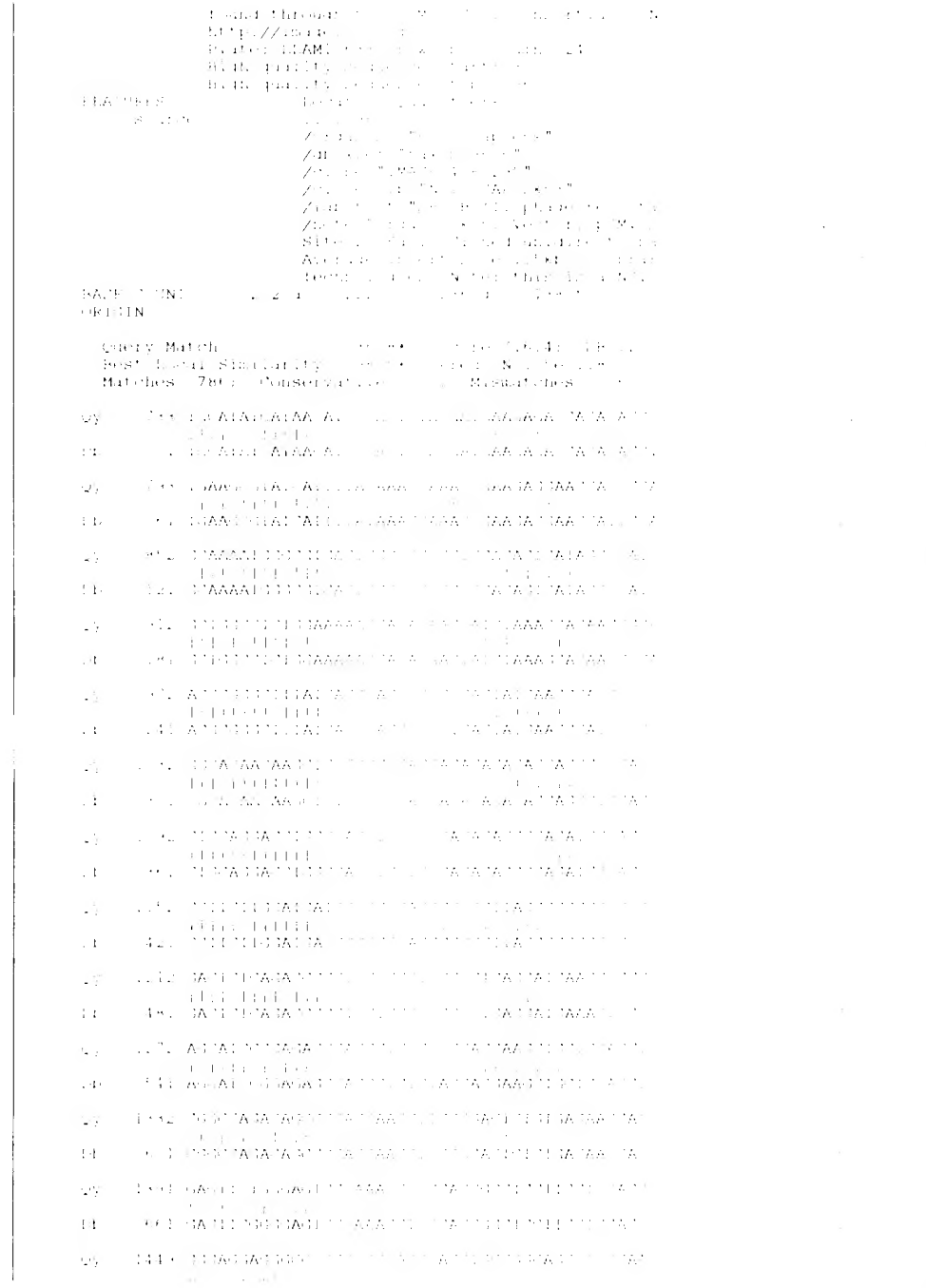
ORIGIN

Query Match 97.5%; Score 761; DB 14; Length 778;
Best Local Similarity 98.1%; Pred. No. 1.6e-126;
Matches 760; Conservative 0; Mismatches 12; Indels 5; Gaps 2;

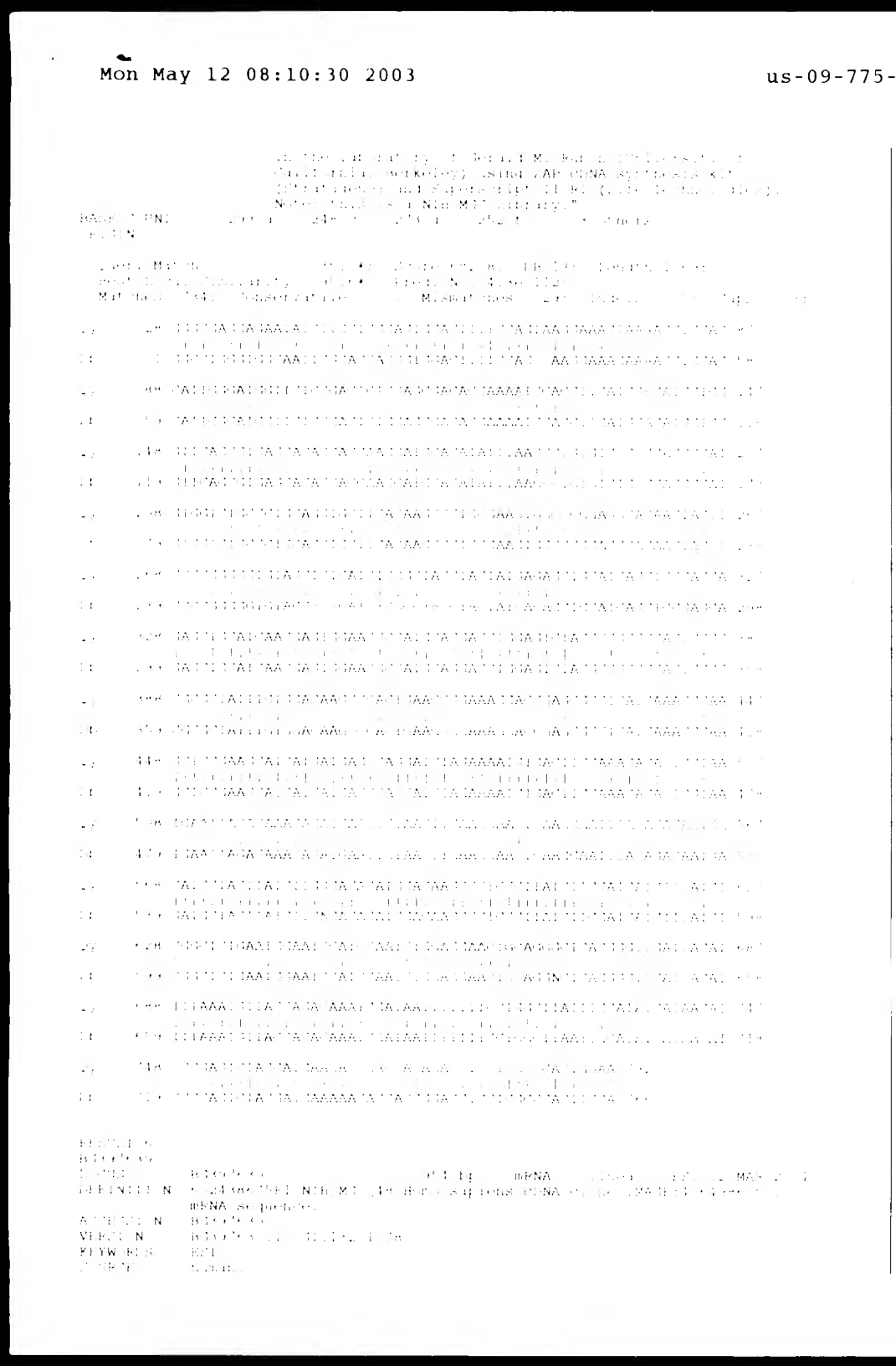
RESULT 2
BM715796
LOCUS BM715796 778 bp mRNA linear EST 29-FEB-2004
DEFINITION BM715796 DI E E30 ah k 16 0 01 5', mRNA sequence.
ACCESSION BM715796
VERSION BM715796.1 GI:19029954
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 778)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
Currently, at Iowa
451 Eckstein Medical Research Building, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9566
Email: address@host.edu
Tissue Procurement: Dr. Gregg Bateman
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequenced by: Dr. M. Bento Soares, University of Iowa
Clone distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 5prime_AluJb (matched complimented)
3seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1..778
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DI E E30"
/clone_lib="DI E E30"
/tissue_type="total - yes, lens, eye anterior segment,
optic nerve, retina, Retina Fovea, and Macular, RPE and
Choroid"
/dev_stage="total and adult"
/lab_host="DH5 (Life Technologies; 2000 Rockville Pike;
Rockville, MD 20852)"
/note="Vector: pCMV-SPORT6; Vector pCMV-SPORT6 was used to
construct this library. Not I Site 1; BssH II; Site 2; Not Ia
DI E E30 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pCMV-SPORT6
vector. The oligonucleotide used to prime the synthesis of
first strand cDNA contains a library bar sequence that is
located between the Not I site and the (dT)n tail. The
sequence 'aagtt' in this library are: 'aagtt' 0; 'aagtt' 1;
lens; CCATAGCGA; eye anterior segment; AATGCCCAT;
optic nerve; CCATAAACG; retina; CCCCC; Retina Fovea and
Macular, GCCC; RPE and Choroid; ACCTA. This library was
created by the program, Selection System, supported by National Eye Institute (NEI)."
BASE COUNT 177 a 230 c 211 g 154 t 6 others
ORIGIN

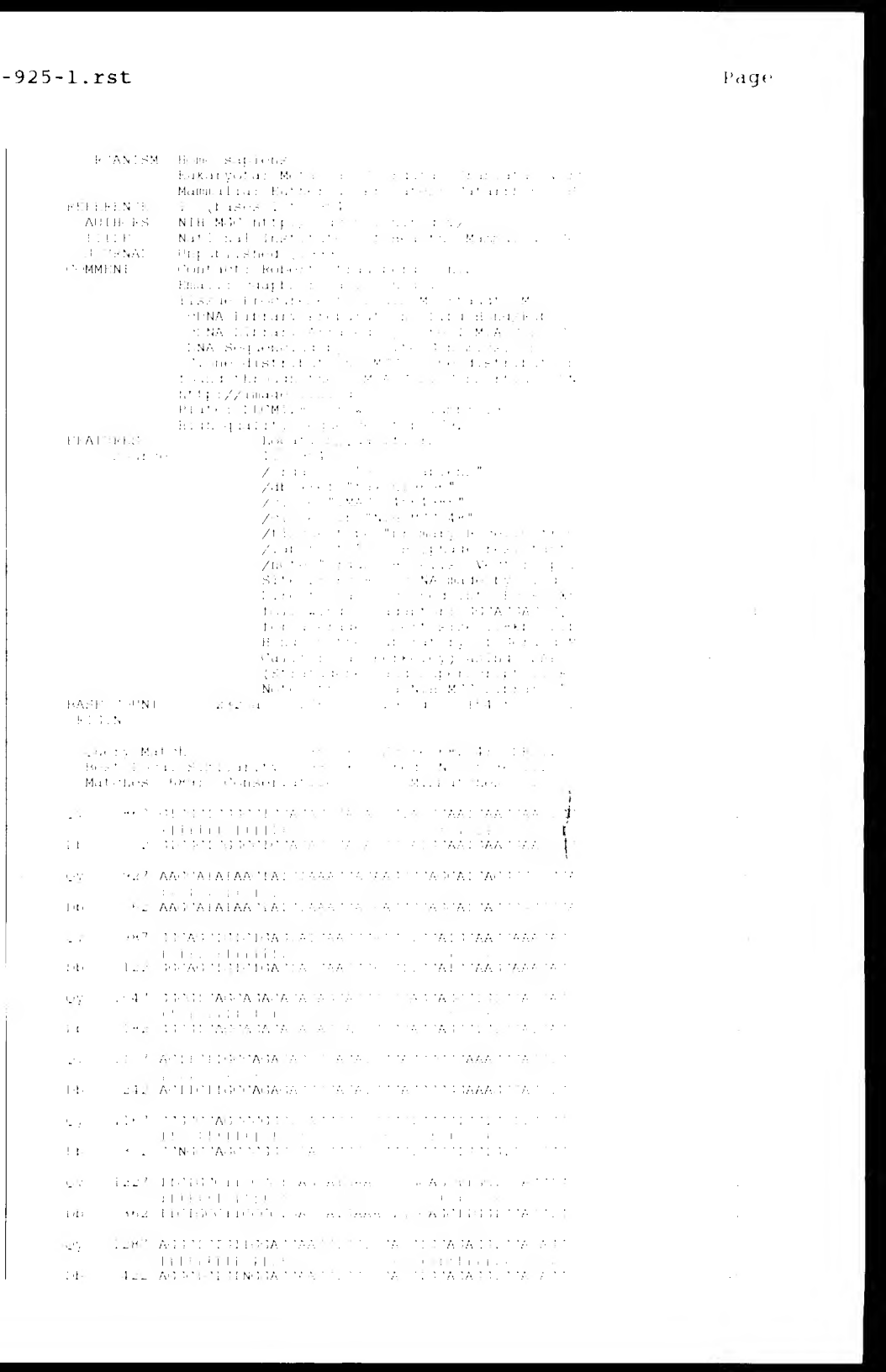
Query Match 97.5%; Score 761; DB 14; Length 778;
Best Local Similarity 98.1%; Pred. No. 1.6e-126;
Matches 760; Conservative 0; Mismatches 12; Indels 5; Gaps 2;

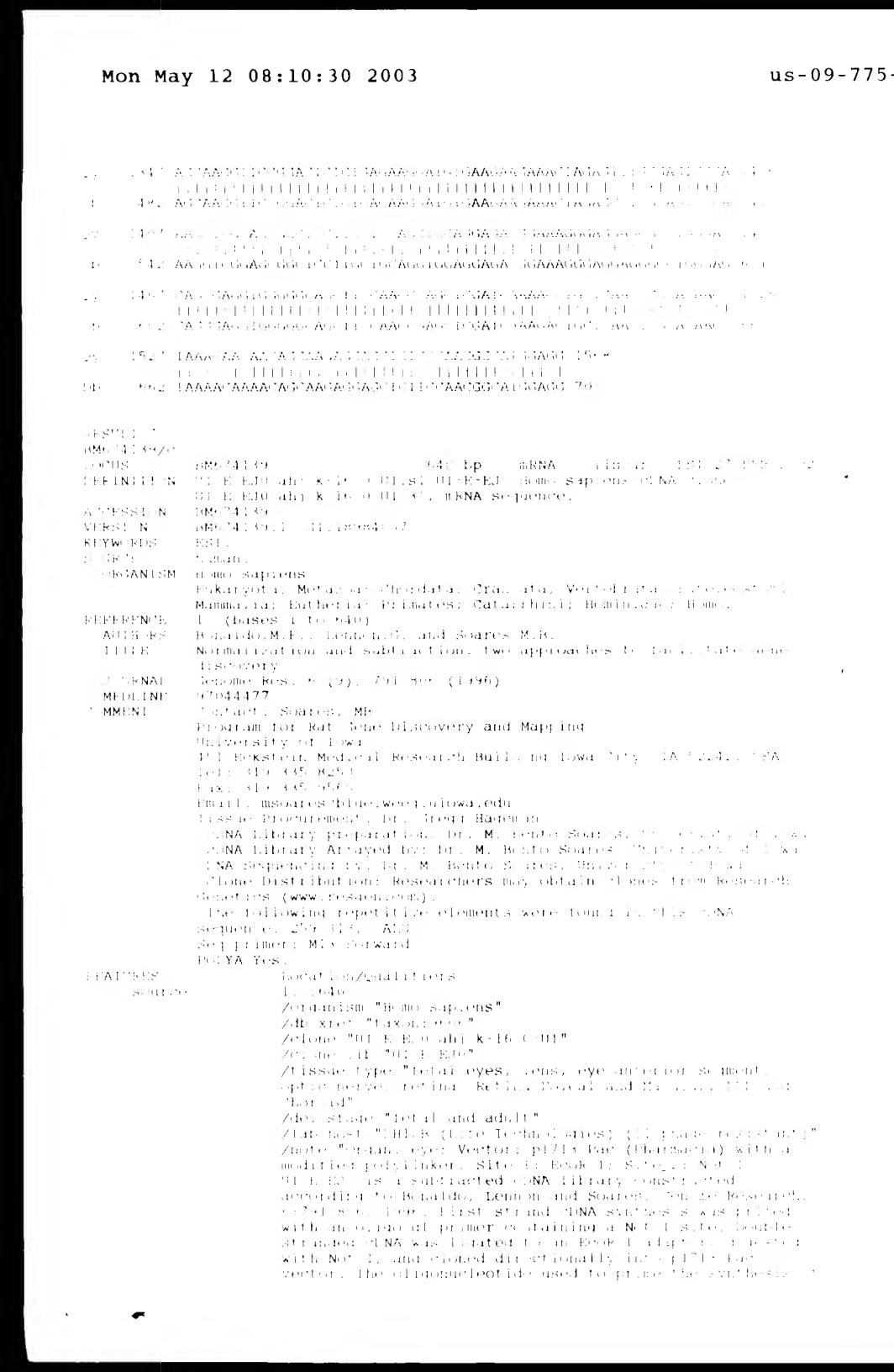




```
LOCUS       BM054754                 708 bp    mRNA    linear   EST 26-FEB-2002
DEFINITION  Homo sapiens cDNA clone IMAGE:5441986 5', mRNA sequence.
ACCESSION   BM054754
VERSION     BM054754.1  GI:18844474
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   NIH MGC http://www.mgc.nih.gov.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cmaps@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Robin Laboratory
            cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Biosciences Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLOML056  row: h  column: 12
            High quality sequence start: 11
            High quality sequence stop: 661.
FEATURES             Location/Qualifiers
     source          1..708
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5441986"
                     /clone_lib="NIH_MGC_98"
                     /tissue_type="astrocytoma, grade IV, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo dT primed; Internally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G); Library constructed by I.M.A.G.E.
```



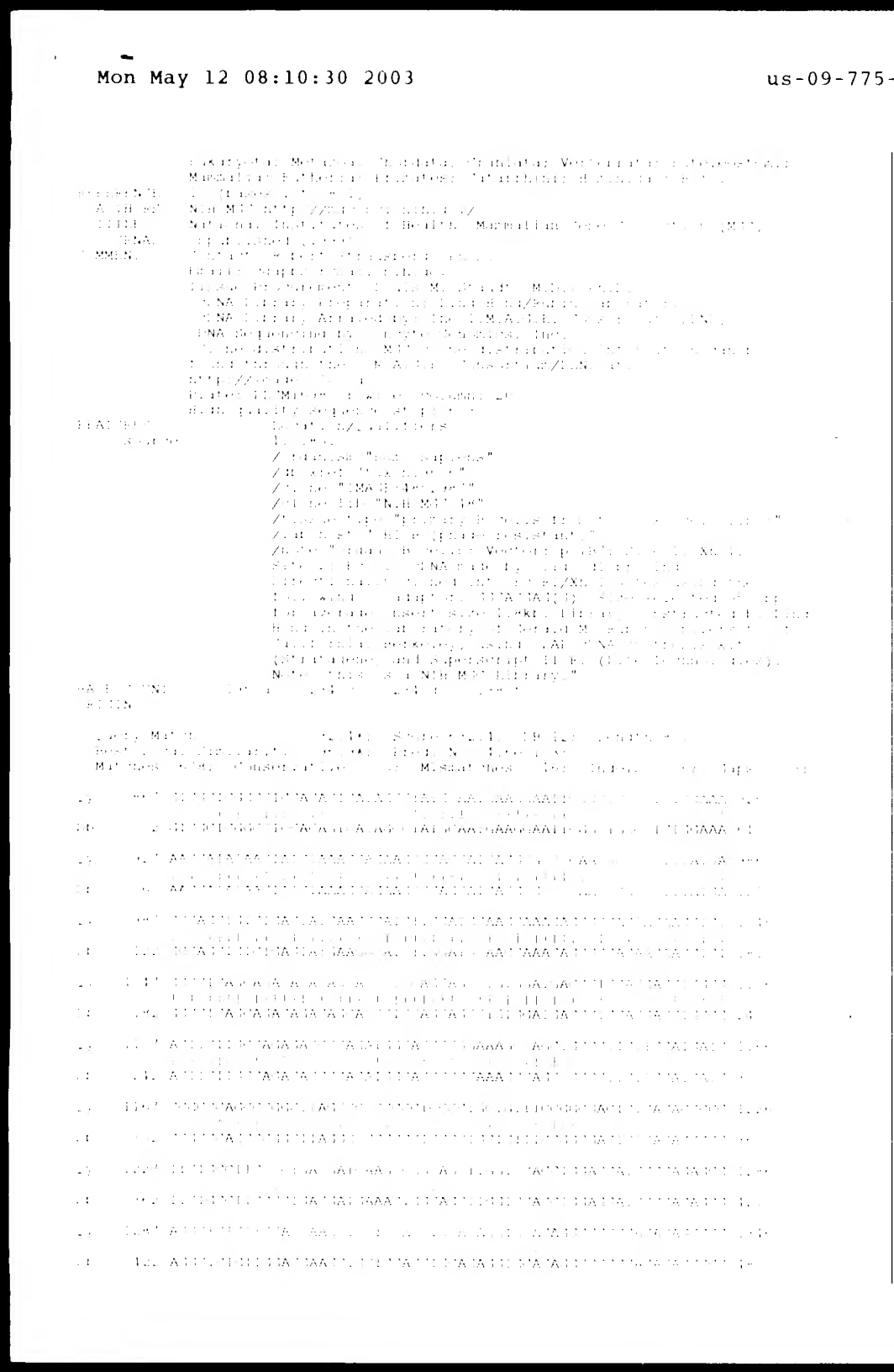


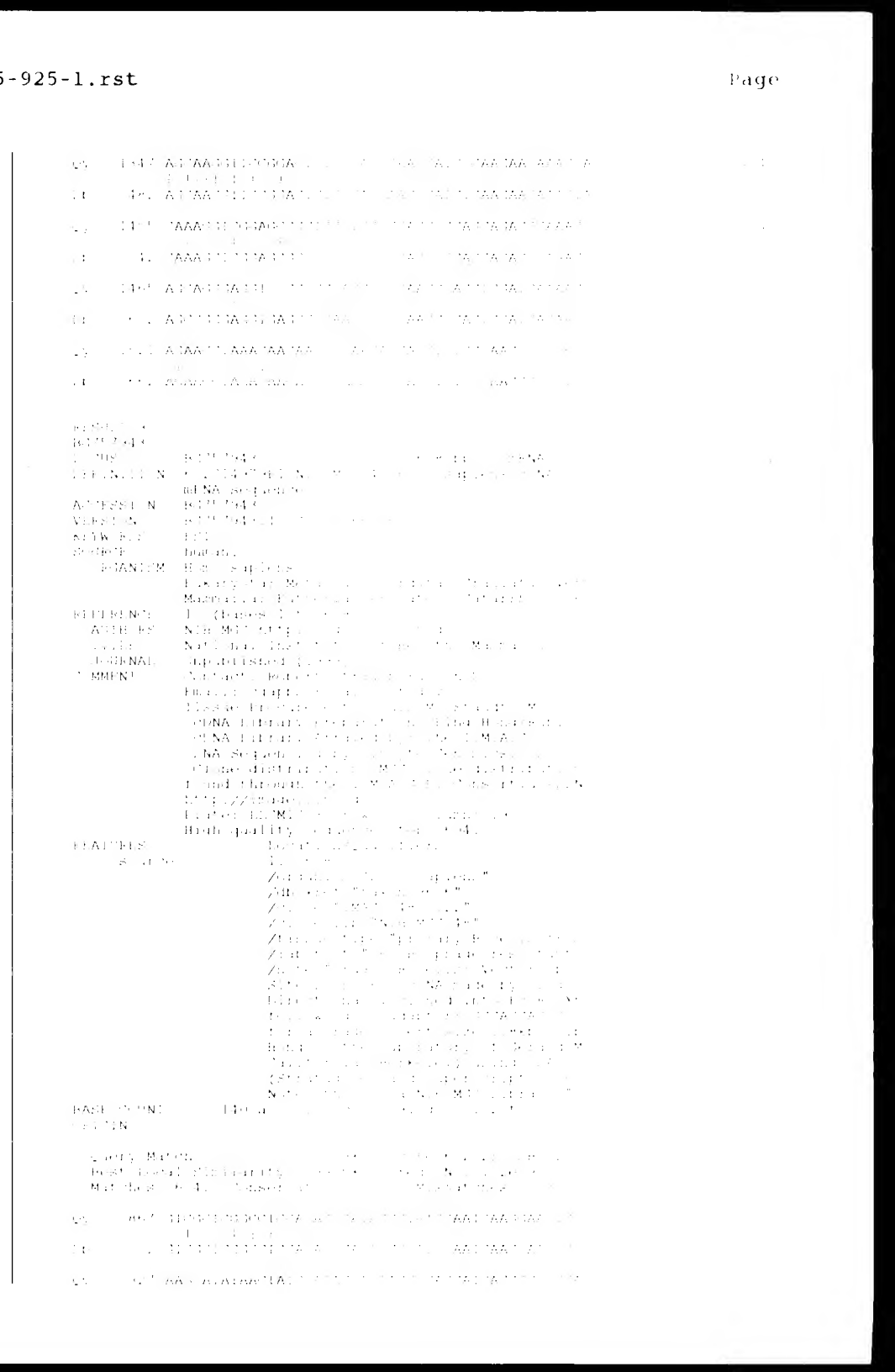


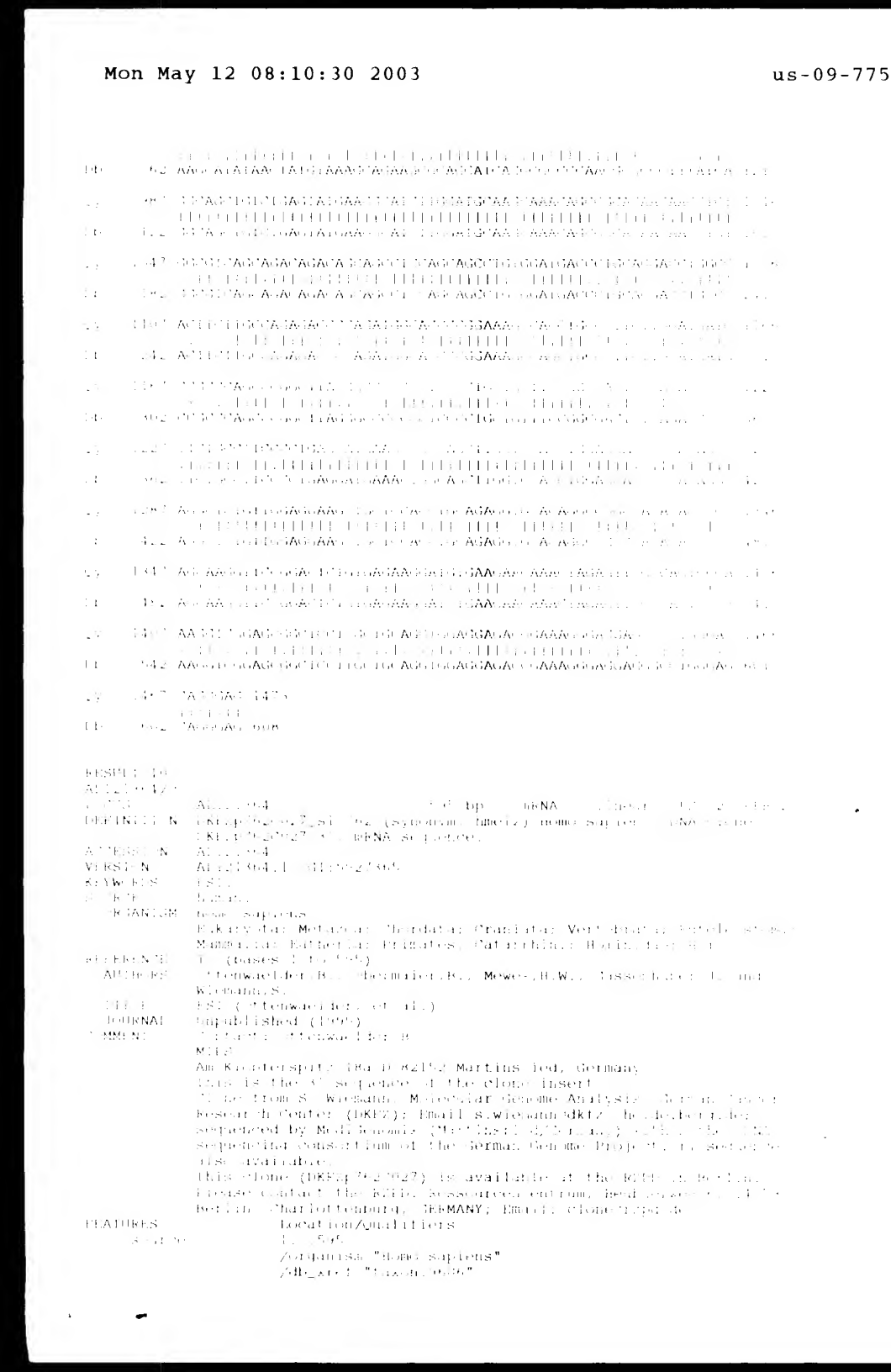
first strand cDNA contains a library of sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAACA ... TCCCC, CCATTAACTG; eye adhesion solution, AAGTCCCATC; optic nerve, CCATTAACTG; retina, CCGCG; fetina Foveal and Macular, CCCC, RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery, at the Vision System, supported by National Eye Institute (NEI).
FAC LIB DI F-EJO
FAC TISSUE RPE and Choroid
FAC SEQ ACCTA"
BASE COUNT 179 a 566 c 171 g 172 t 1 others
ORIGIN

Query Match 42.8%; Score 649; DB 14; Length 569;
Best Local Similarity 99.8%; Pred. No. 3.4e-104;
Matches 639; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LOCUS BM974139 642 bp mRNA linear EST 27-MAY-2002
DEFINITION yy E EJ0 ahi k-16 c-01, mRNA sequence.
ACCESSION BM974139
VERSION BM974139.1 GI:11069207
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 642)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
301 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8259
Fax: 319 335 9006
Email: mbsoares-bioc@uiowa.edu
Tissue Procurement: Dr. Joseph Bardwell
cDNA Library preparation: Dr. M. Bento Soares, Dr. Ivette Zeva
cDNA Library Arrayed by: Dr. M. Bento Soares
DNA Sequencing by: Dr. M. Bento Soares, Bruce J. Mayer
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 2?? SINE: ALU
Seq primer: M13 forward
POLYA Yes.
FEATURES location/qualifiers
source 1..642
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3485087"
/clone_lib="NCI_E_EJ0"
/tissue_type="fetal eyes, lens, eye adhesion solution, optic nerve, retina, Retina, Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies)"
/note="retina, eyes; Vector: pT7T3 Pac (Pharmacia) with a modified polylinker; Site 1: Eco0 I; Site 2: Not I
NCI_E_EJ0 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo dT primer containing a Not I site. Double stranded cDNA was digested to an Eco0 I adaptor, Sfi I digested with Not I, and cloned directionally into pT7T3 Pac vector. The oligonucleotide used to prime the synthesis"







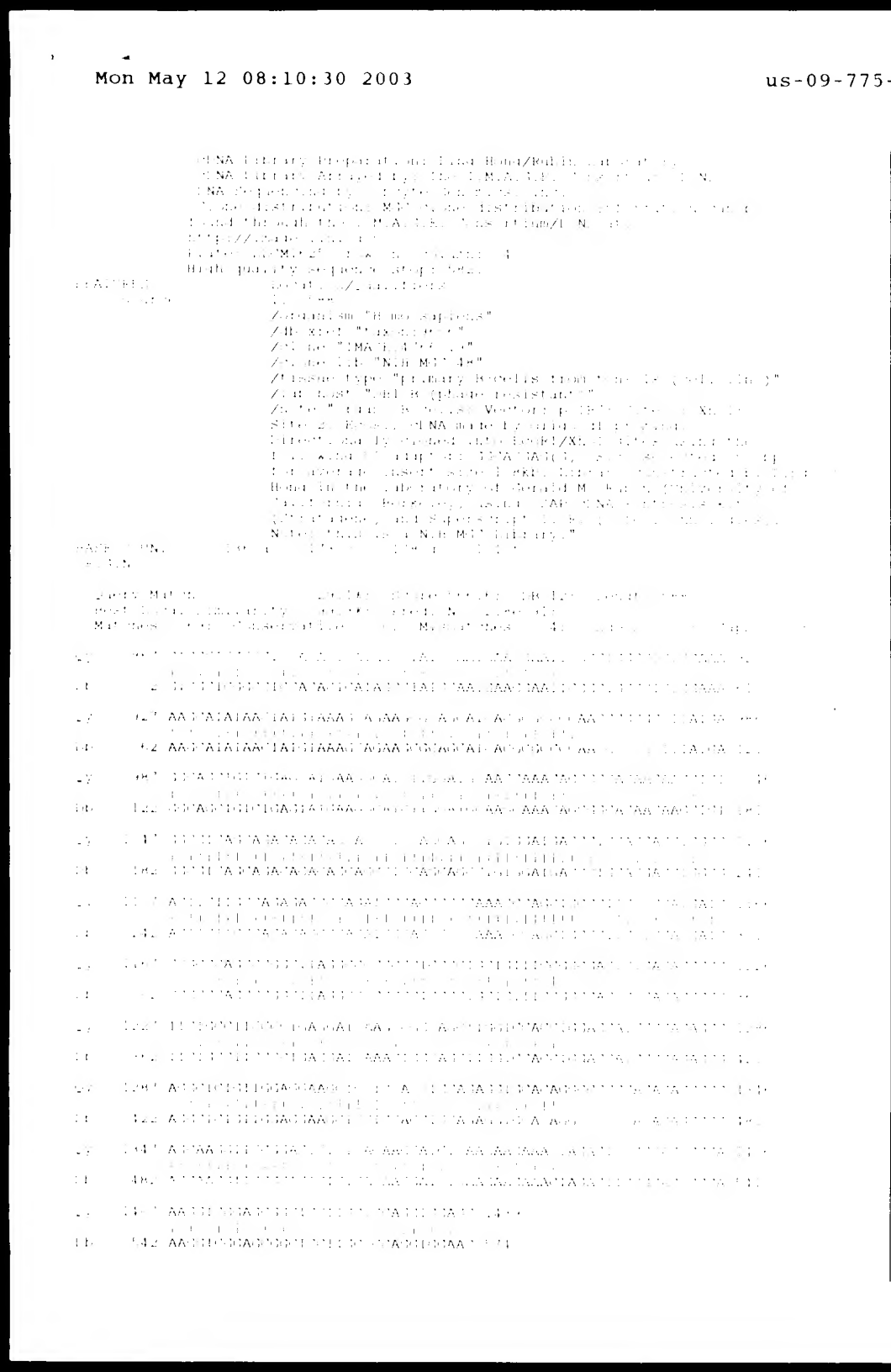
/clone "DKFZp762O027"
/clone_lib "7x2 (synonyms: hmel2)"
/tissue_type "melanoma (MeWo cell line)"
/dev_stage "adult"
/lab_host "DH10B"
/note "vector: pOTB7; Not Site: Sal1"
BASE COUNT 117 a 168 c 158 g 142 t
ORIGIN

Query Match 30.4%; Score 1.8; DB 9; Length 5'-3'
Best Local Similarity 99.7%; Pred. No. 8.9e-05;
Matches 5'-3', Conservative 0; Mismatches 2; Indels 0; Gaps 0;

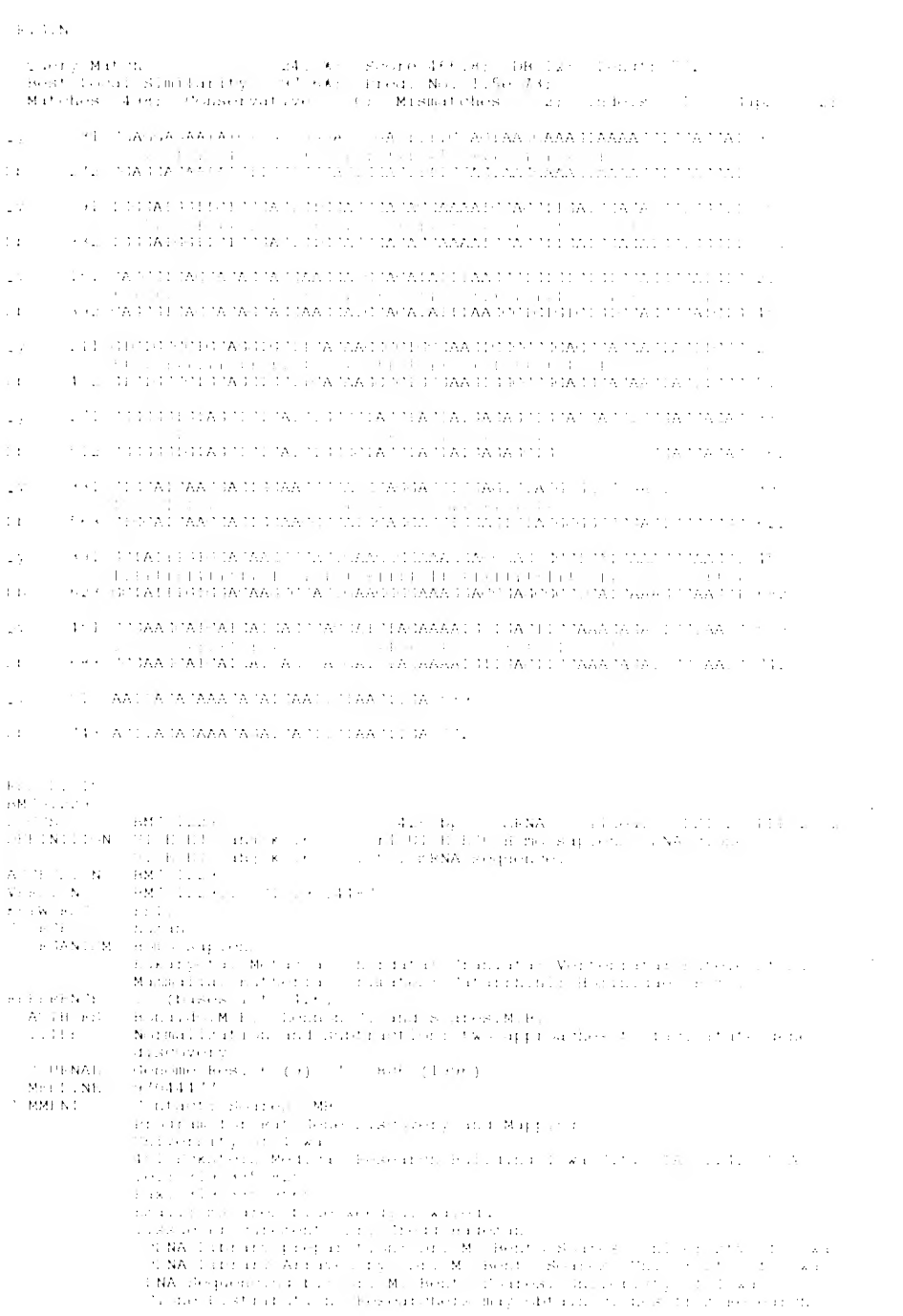
RESULT 10
AC122042
LOCUS AC122042 [illegible] bp mRNA [illegible]
DEFINITION Homo sapiens clone DKFZp762O027 [illegible] mRNA sequence.
ACCESSION AC122042
VERSION AC122042.1 GI:29725
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5'-3')
AUTHORS Stanke,M., Steinkamp,R., Waack,S. and Morgenstern,B.
TITLE AUGUSTUS: a web server for gene finding in eukaryotes
JOURNAL Nucleic Acids Res. 32 (Web Server issue), W309-W312 (2004)
MEDLINE 15215400
PUBMED 15215400
REFERENCE 2 (bases 1 to 5'-3')
AUTHORS Stanke,M. and Waack,S.
TITLE Gene prediction with a hidden Markov model and a new intron submodel
JOURNAL Bioinformatics 19 Suppl 2, II215-II225 (2003)
MEDLINE 14534192
PUBMED 14534192
REFERENCE 3 (bases 1 to 5'-3')
AUTHORS Stanke,M., Steinkamp,R., Waack,S. and Morgenstern,B.
TITLE AUGUSTUS: a web server for gene finding in eukaryotes
JOURNAL Unpublished (2004)
COMMENT Contact: Mario Stanke
Email: mario.stanke@gmx.de
Address: Am Kreuzbergstr. 19a D-37075 Martinus Ied, Germany
This is the 3' sequence of the clone insert
5' is from S. Wiesand, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiesand@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried, Germany); e-mail: info@medigenomix.de;
sequencing consortium of the German Genome Project; for Service
use available.
This clone (DKFZp762O027) is available at the RZPD in Berlin
Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, D-14059
Berlin, Charlottenburg, GERMANY; Email: clone@rzpd.de
FEATURES Location/Qualifiers
source 1..5'-3'
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762O027"
/clone_lib="7x2 (synonyms: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="vector: pOTB7; Not Site: Sal1"
BASE COUNT 117 a 168 c 158 g 142 t
ORIGIN

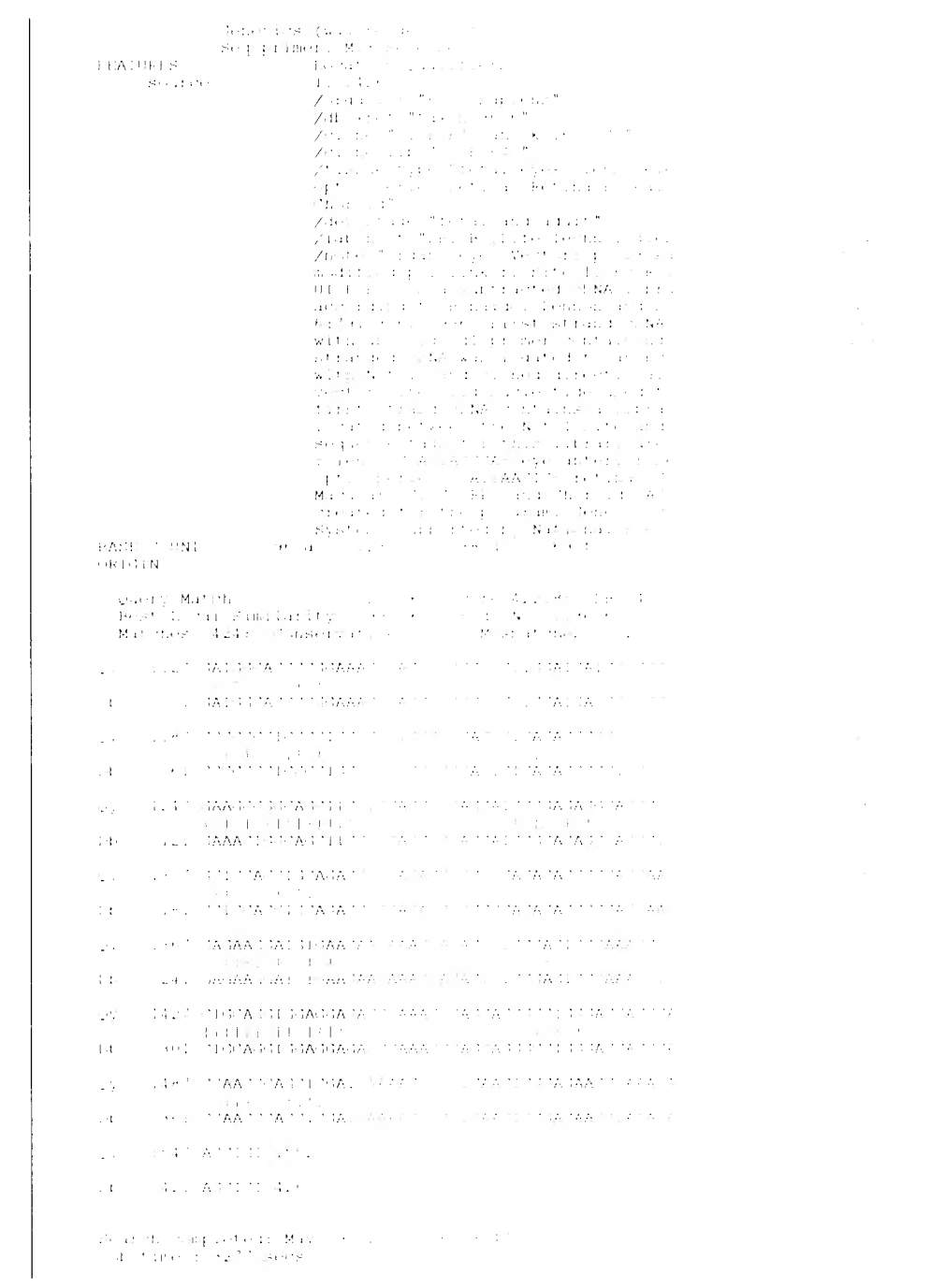
Query Match 30.4%; Score 1.8; DB 9; Length 5'-3'
Best Local Similarity 99.7%; Pred. No. 8.9e-05;
Matches 5'-3', Conservative 0; Mismatches 2; Indels 0; Gaps 0;

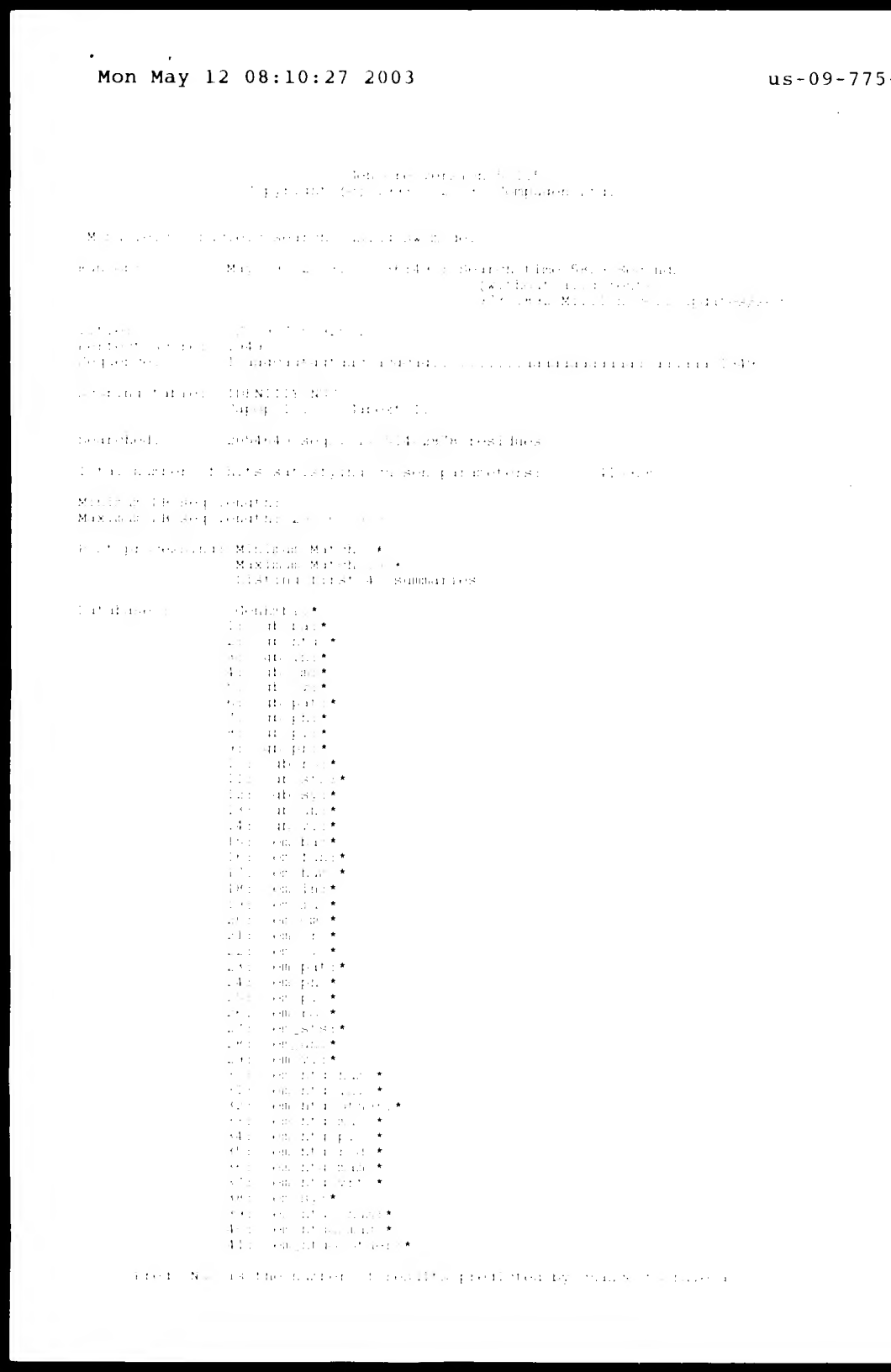
RESULT 11
BC086304
LOCUS BC086304 5'-3' bp mRNA linear EST 31-MAY-2004
DEFINITION Homo sapiens, clone MGC:[illegible] IMAGE:[illegible], mRNA sequence.
ACCESSION BC086304
VERSION BC086304.1 GI:[illegible]
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5'-3')
AUTHORS [illegible]
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Louis M. Staudt, M.D., Ph.D.

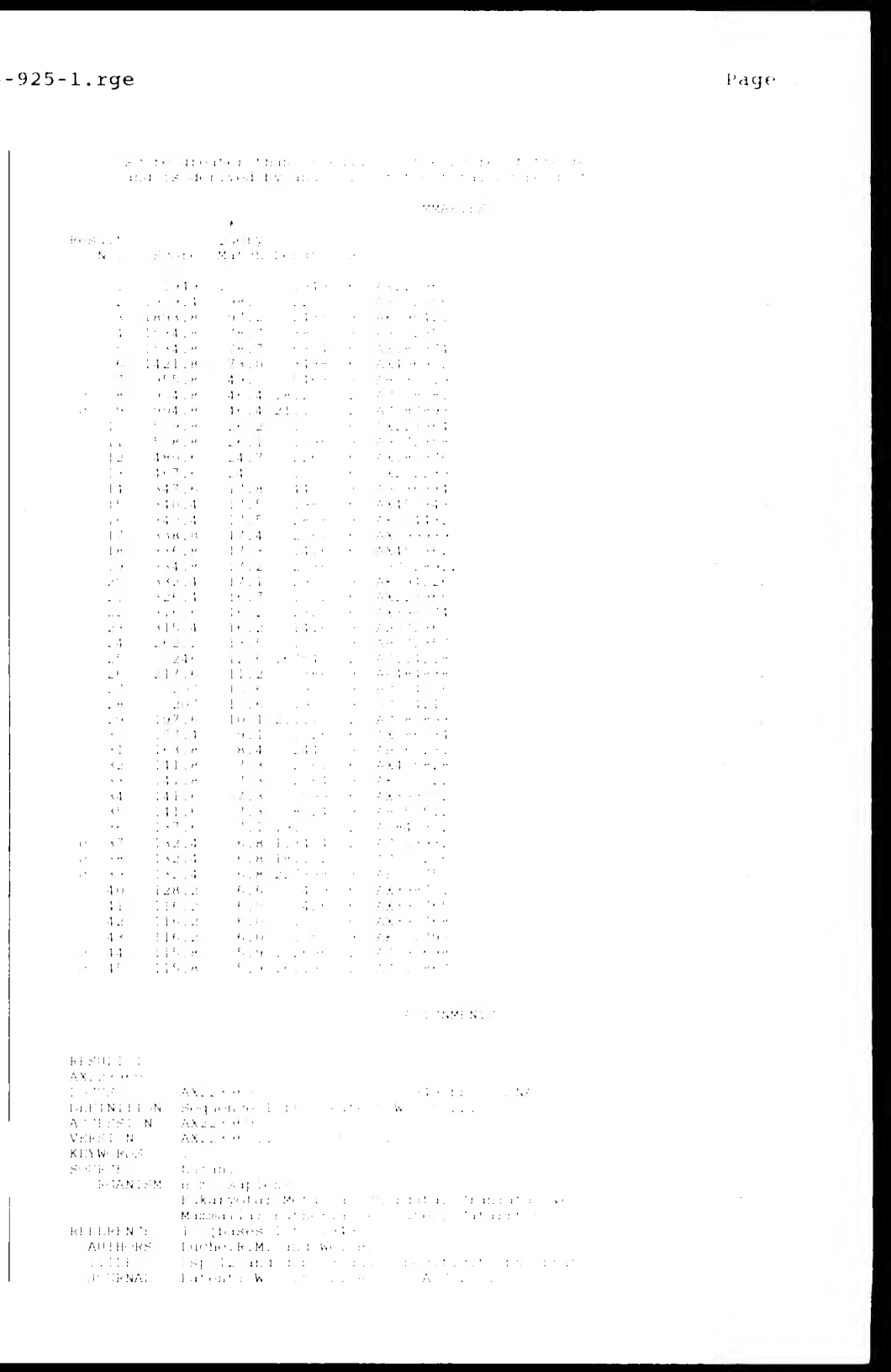


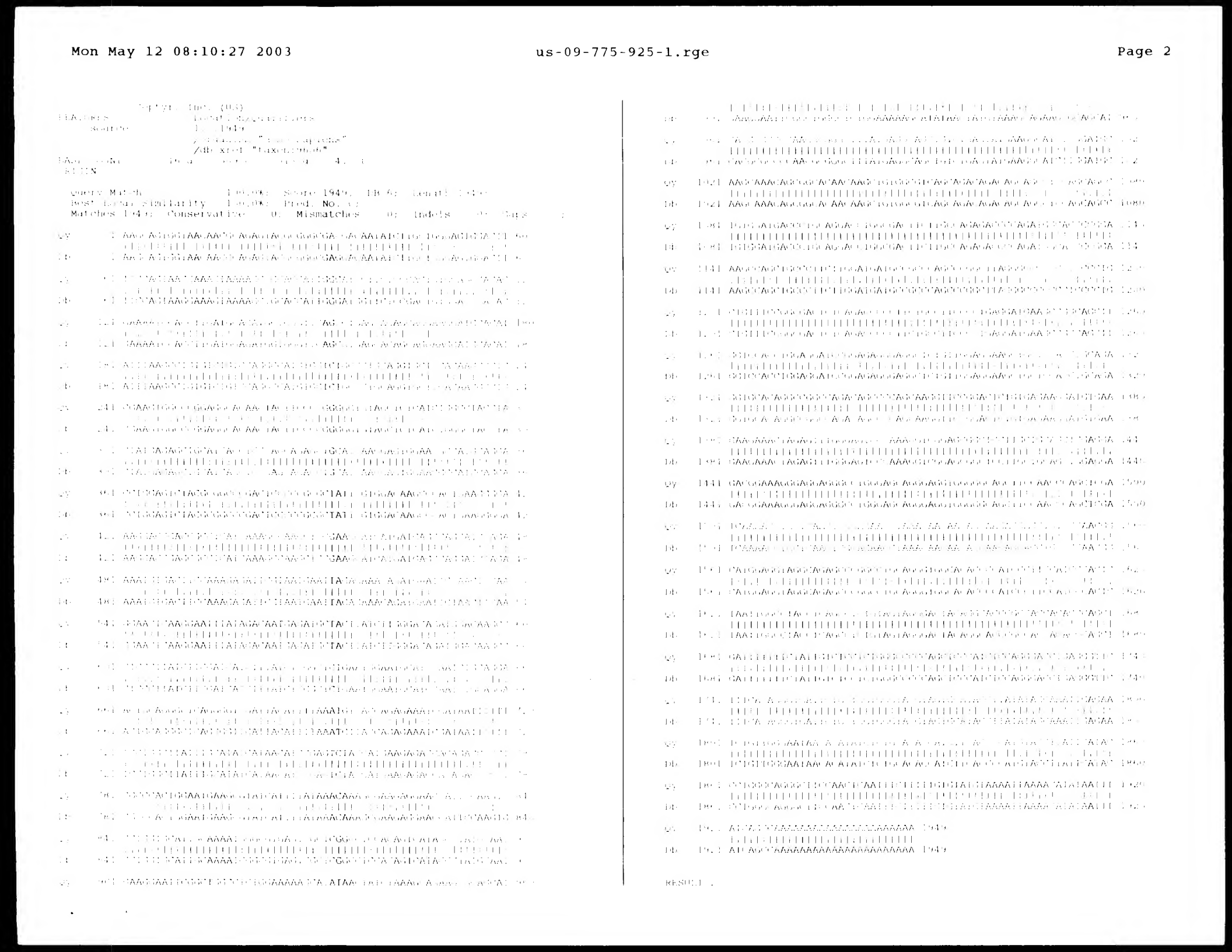
RESULT 12
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BASE COUNT
ORIGIN



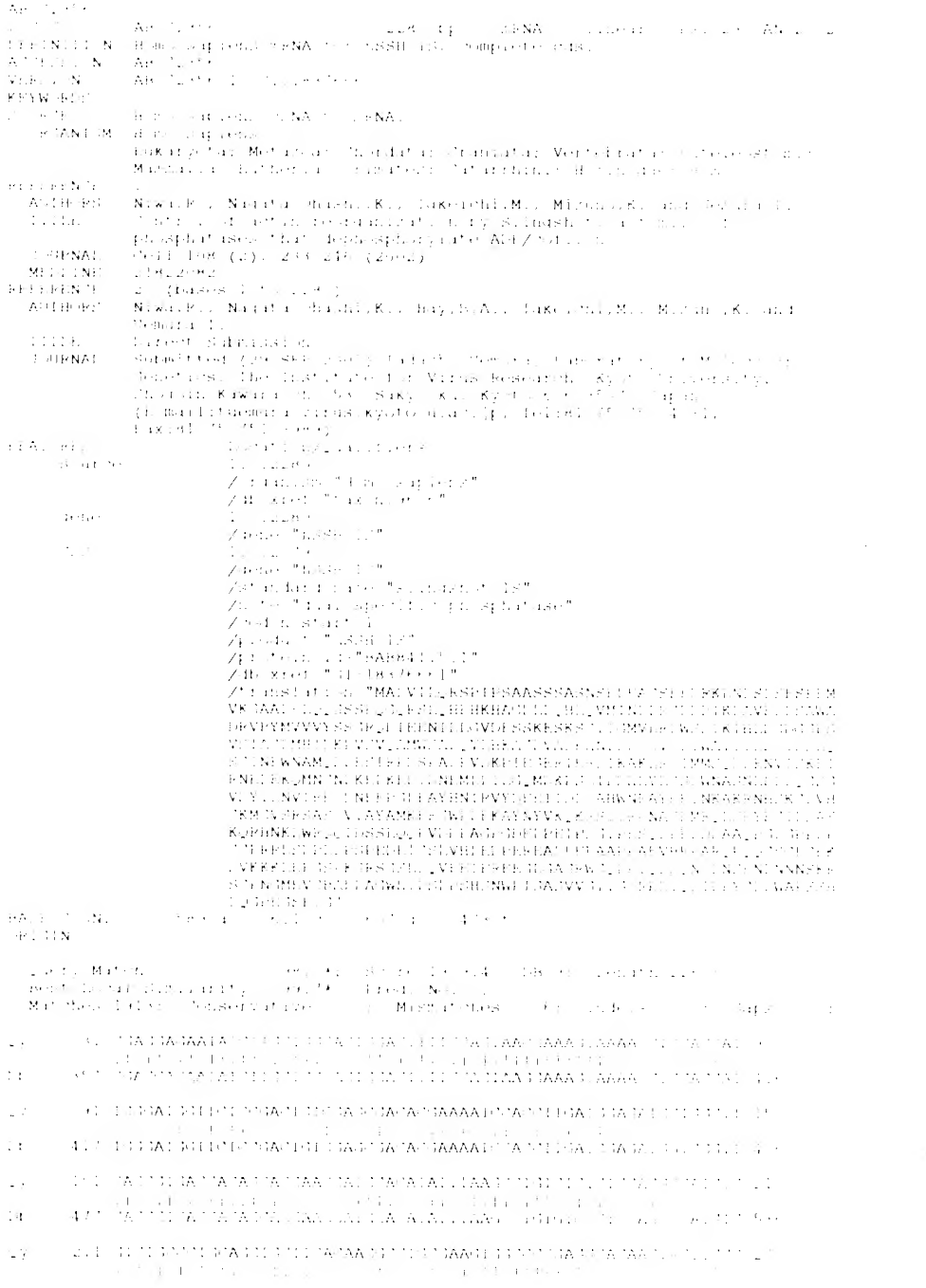


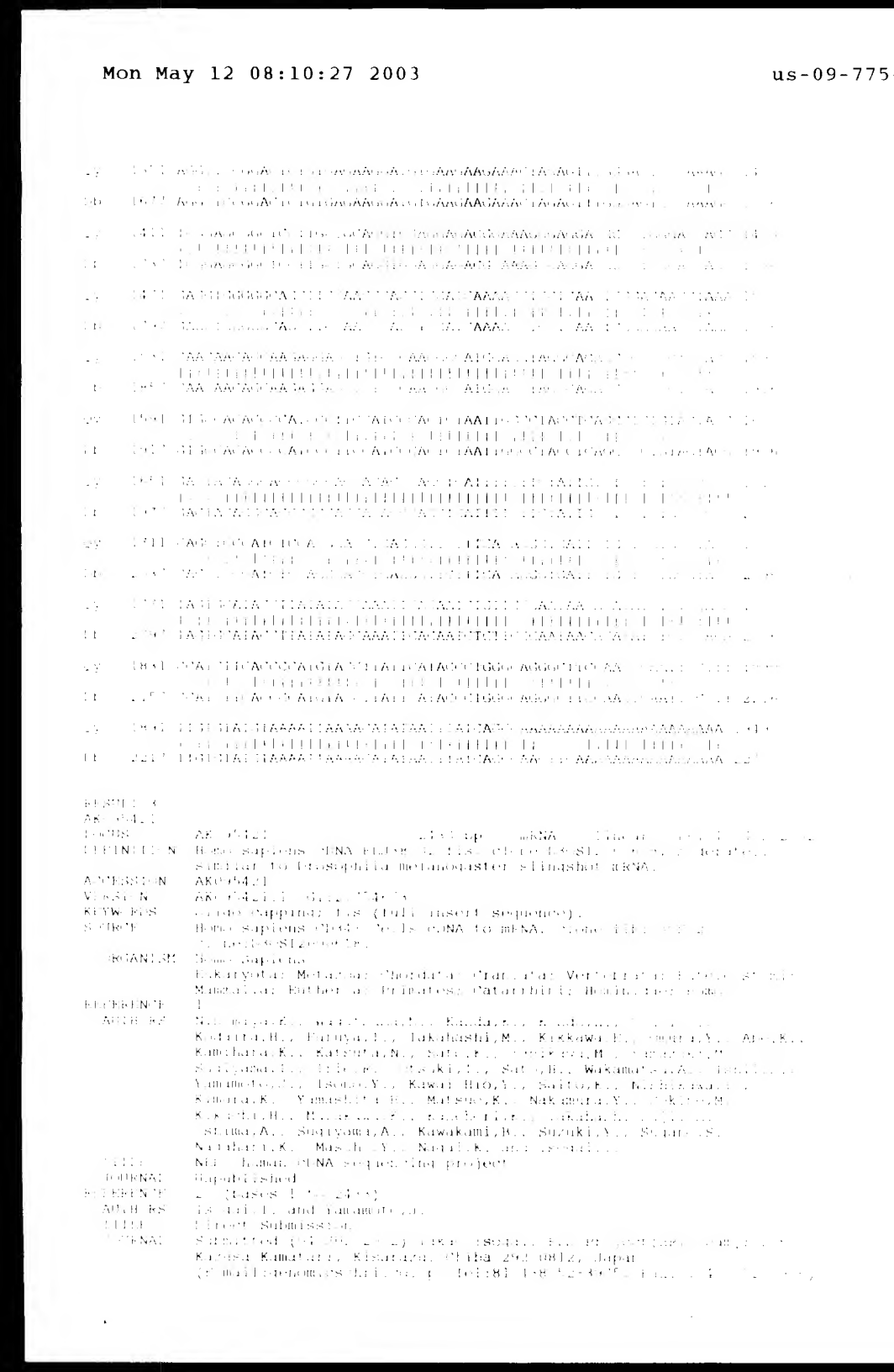






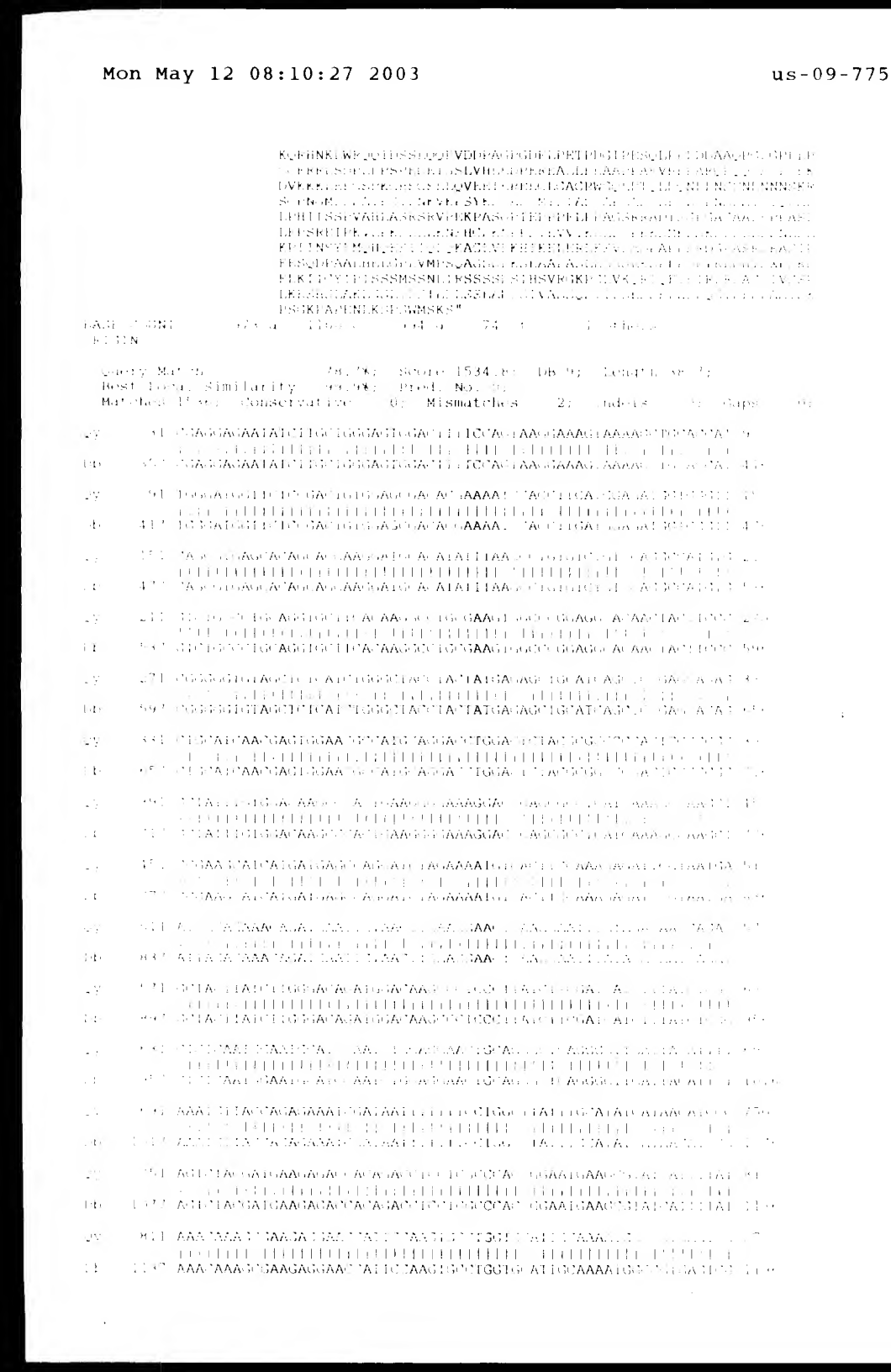
RESULT 1

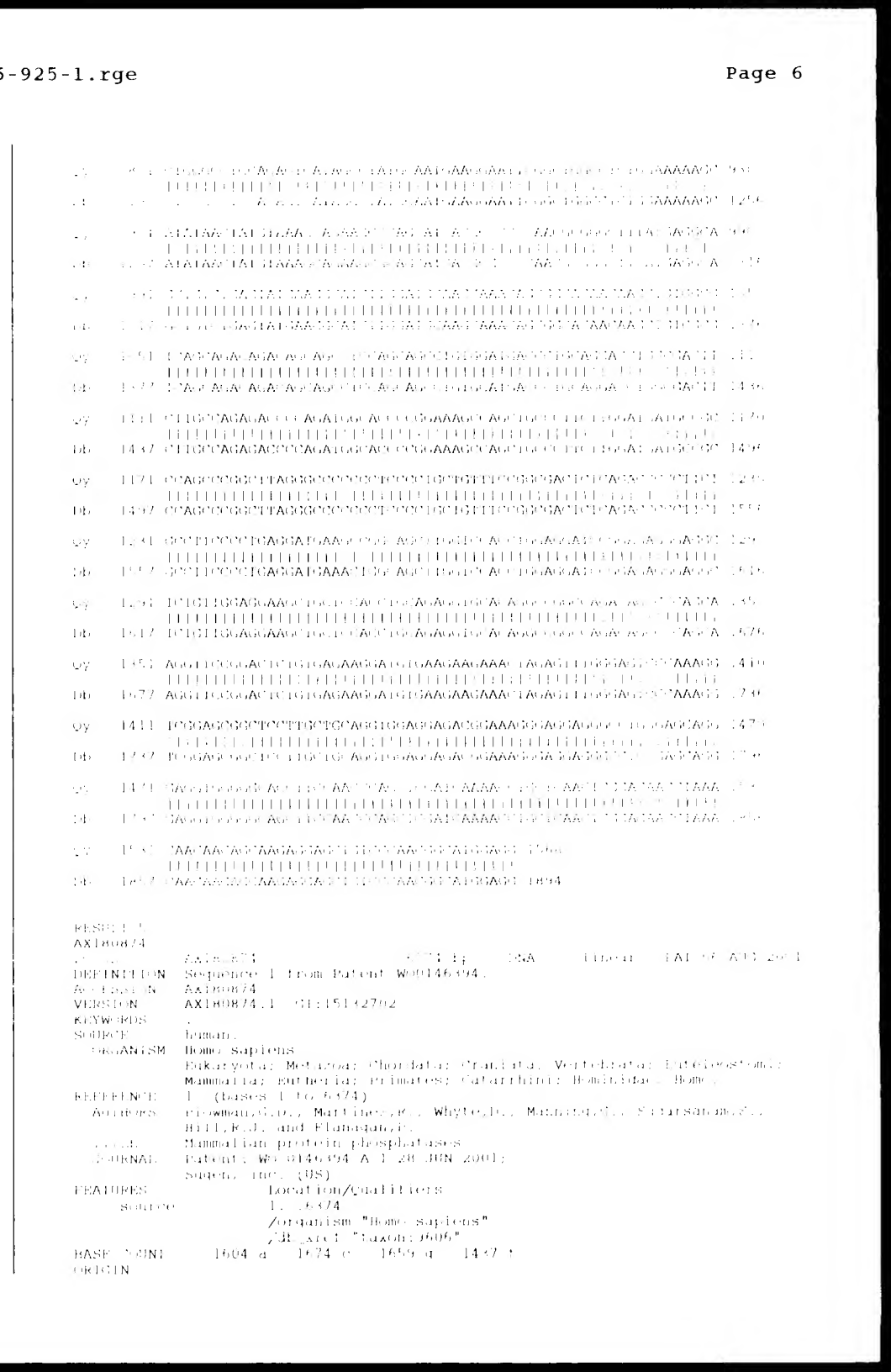


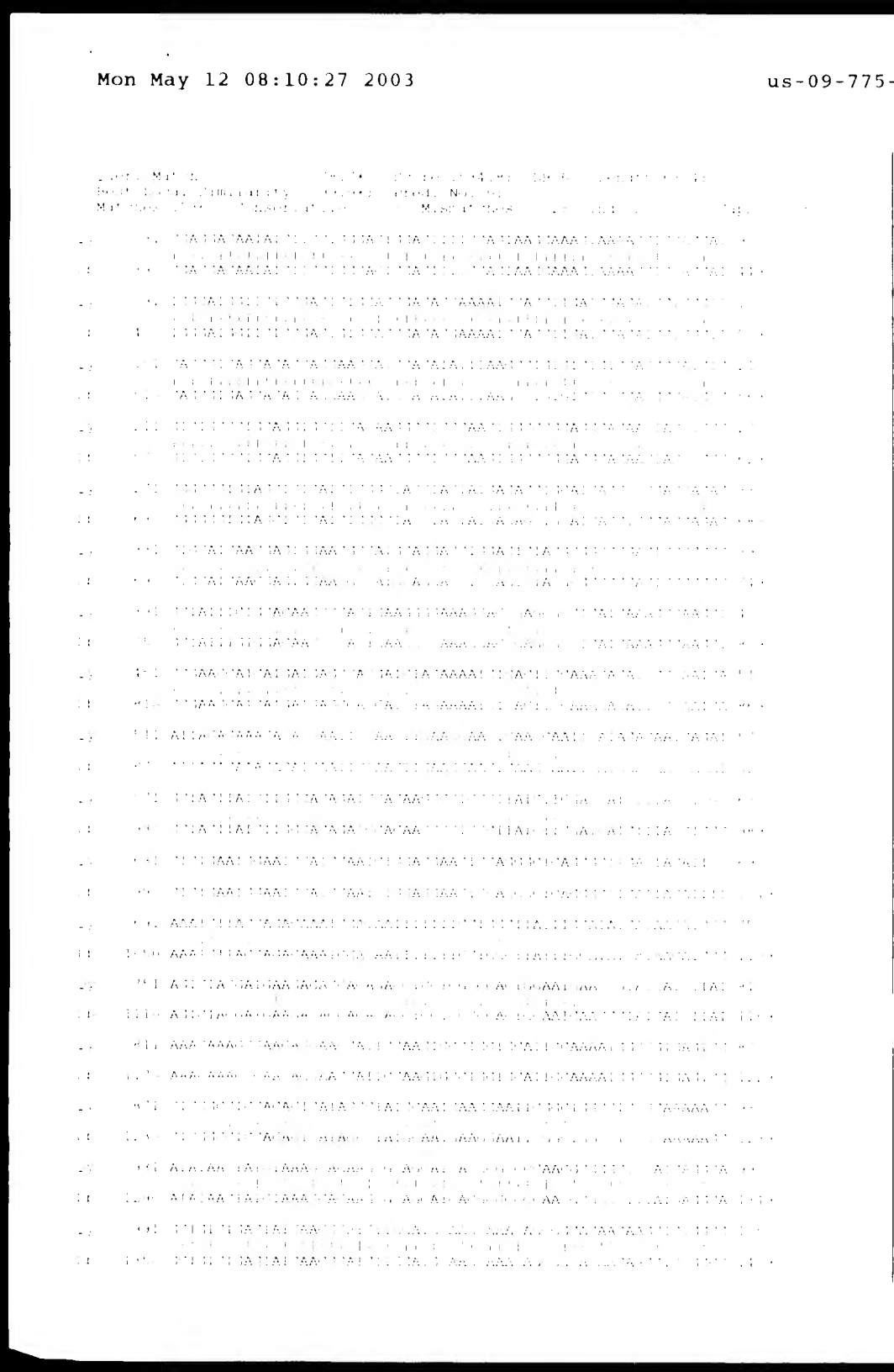


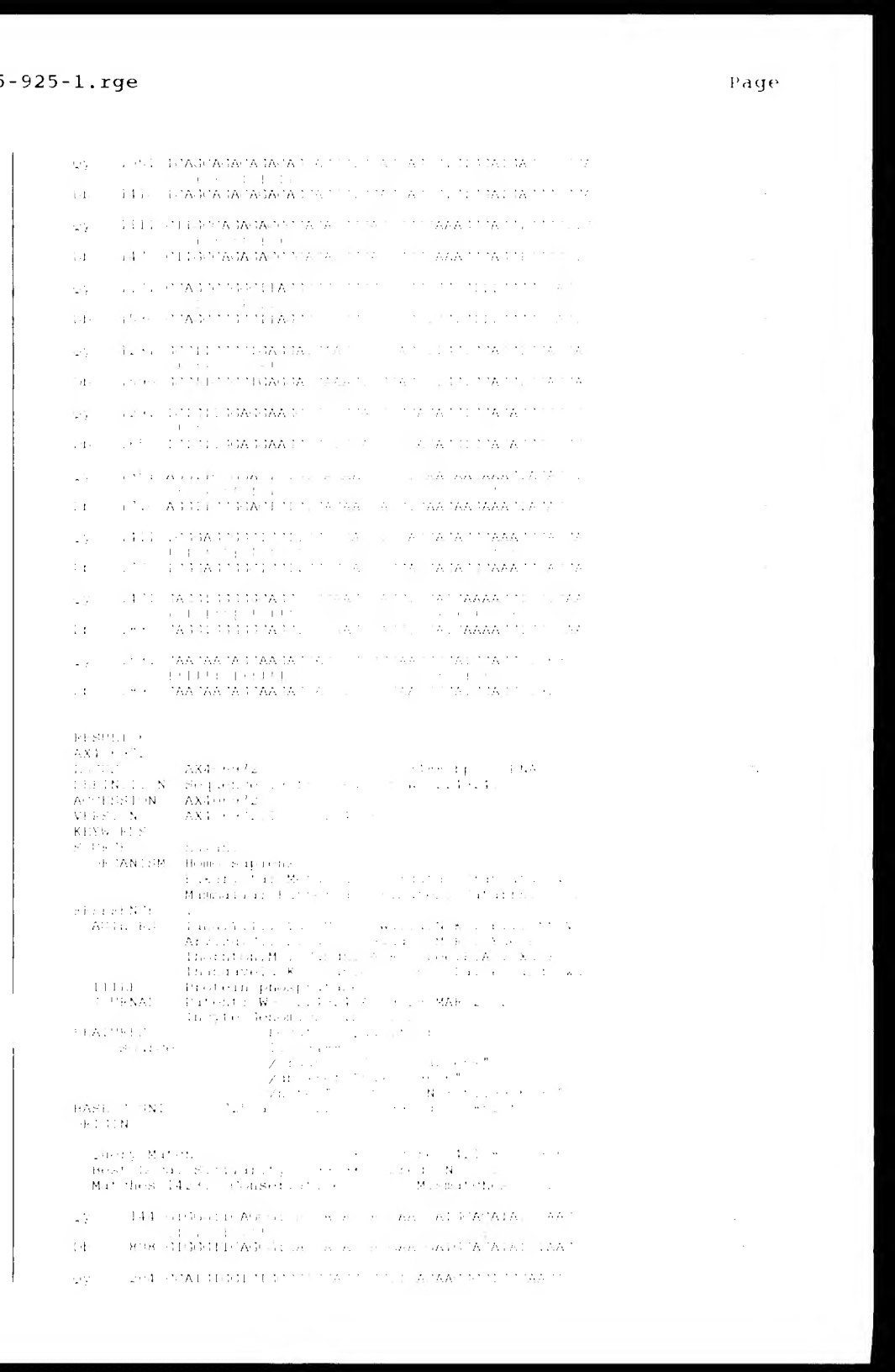
[illegible]

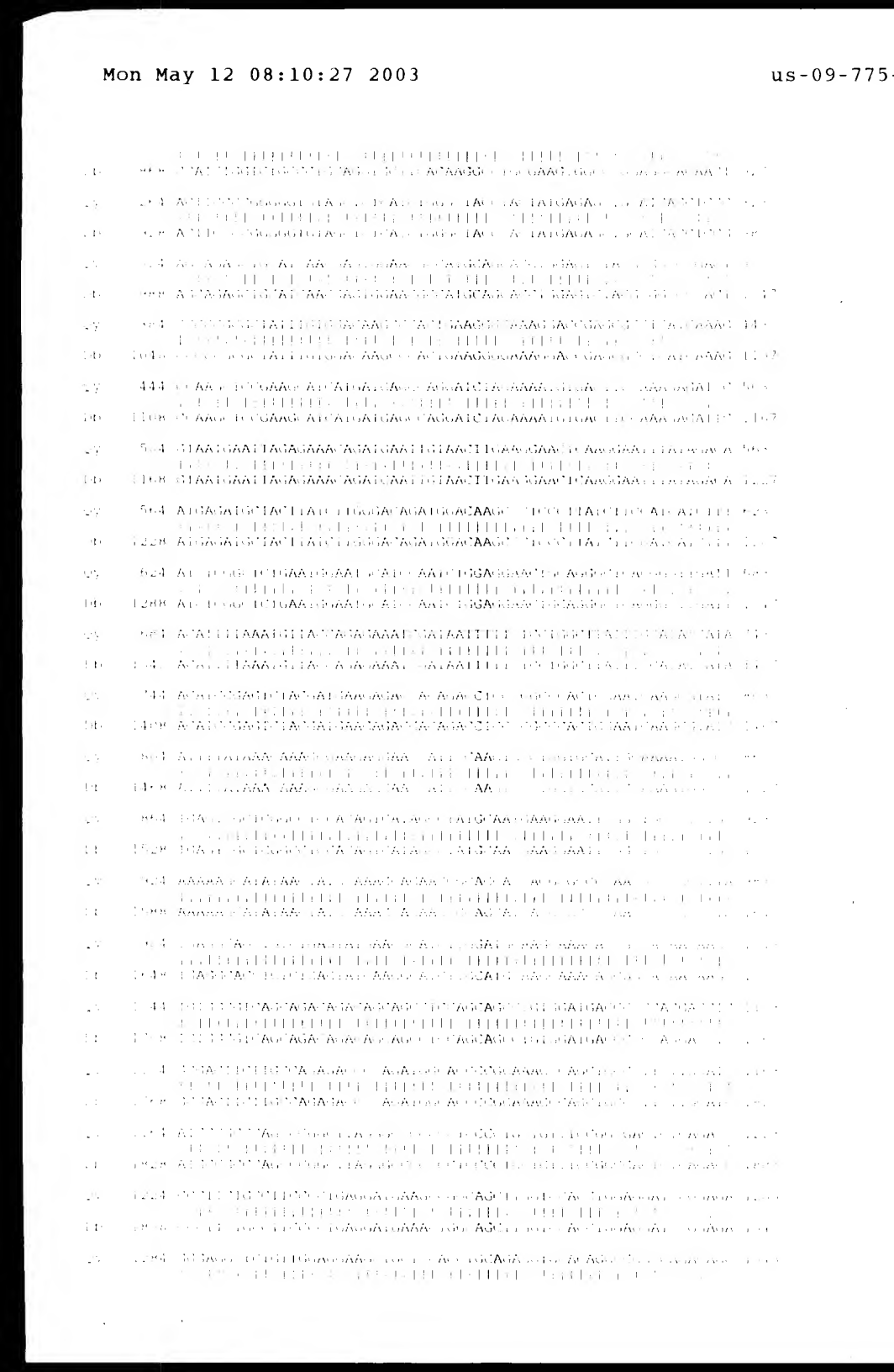
RESULT 4
[illegible]
DEFINITION Homo sapiens [illegible]
VERSION [illegible]
SOURCE Homo sapiens [illegible]
ORGANISM Homo sapiens
Eukaryota; [illegible]
Mammalia; [illegible]
REFERENCE 1
AUTHORS [illegible]
TITLE [illegible]
JOURNAL [illegible]
MEDLINE [illegible]
REFERENCE 2 (bases [illegible])
AUTHORS [illegible]
TITLE Direct Submission
JOURNAL Submitted [illegible]
[illegible]
FEATURES Location/Qualifiers
[illegible]











RESULT 7
AB037719
LOCUS AB037719 5463 bp mRNA linear PRI 14-MAR-2000
DEFINITION Homo sapiens mRNA for KIAA1298 protein, partial cds.
ACCESSION AB037719
VERSION AB037719.1 GI:7242950
KEYWORDS .
SOURCE Homo sapiens brain cDNA to mRNA, clone:hp04206, pBluescriptII SK plus
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
REFERENCE 1 (bases 1 to 5463)
AUTHORS Nagase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes.
XVI. The complete sequences of 150 new cDNA clones from brain which
code for large proteins in vitro
JOURNAL DNA Res. 7 (1), 65-73 (2000)
MEDLINE 20141126
REFERENCE 2 (bases 1 to 5463)
AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1999) Laboratory of DNA Technology, 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:dnadata@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:+81 438 52 3934,
Fax:+81 438 52 3914)
FEATURES Location/Qualifiers
source 1..5463
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hp04206"
/tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
gene 1..5463
/gene="KIAA1298"
CDS 536..12272
/gene="KIAA1298"
/note="Start codon is not identified."
/codon_start=1
/product="KIAA1298 protein"
/protein_id="BAA25536.1"
/db_xref="GI:7242951"
/translation="MPWYCDWSWGVPLLLLLLVSSLVVGVPEENVIRELNEIFGIAY
NNSVFDLVNKLRKHLNITNKTMKLLSTLDLDAKLPPKCGMQRLDLCLLLVC
HPAQVSRTACPEGSVCYEKSVDLTLNWNAQNPGLGPPLEYKLFWFRELSDPLLPSPEHDSSI
VHLEDPEREALLEEAAITVAAGLVIVIFVMLFLFLWKLGRSGKHKNSKLSV
DLTNIDEMDDSWAGLRSENFIYDEQLPGQDETLVGNLMKSNVCIQRLPTQ
YRLAGVKKSLLYLLIKDVDKVNKCILGEKIKFLMNLEIPFCKLQFCDKIPI
GSQEKSEAAFKSLRSQLEKSPGEYRLHGIESGSLKEDLKLSPLSSGMSVNLTDS
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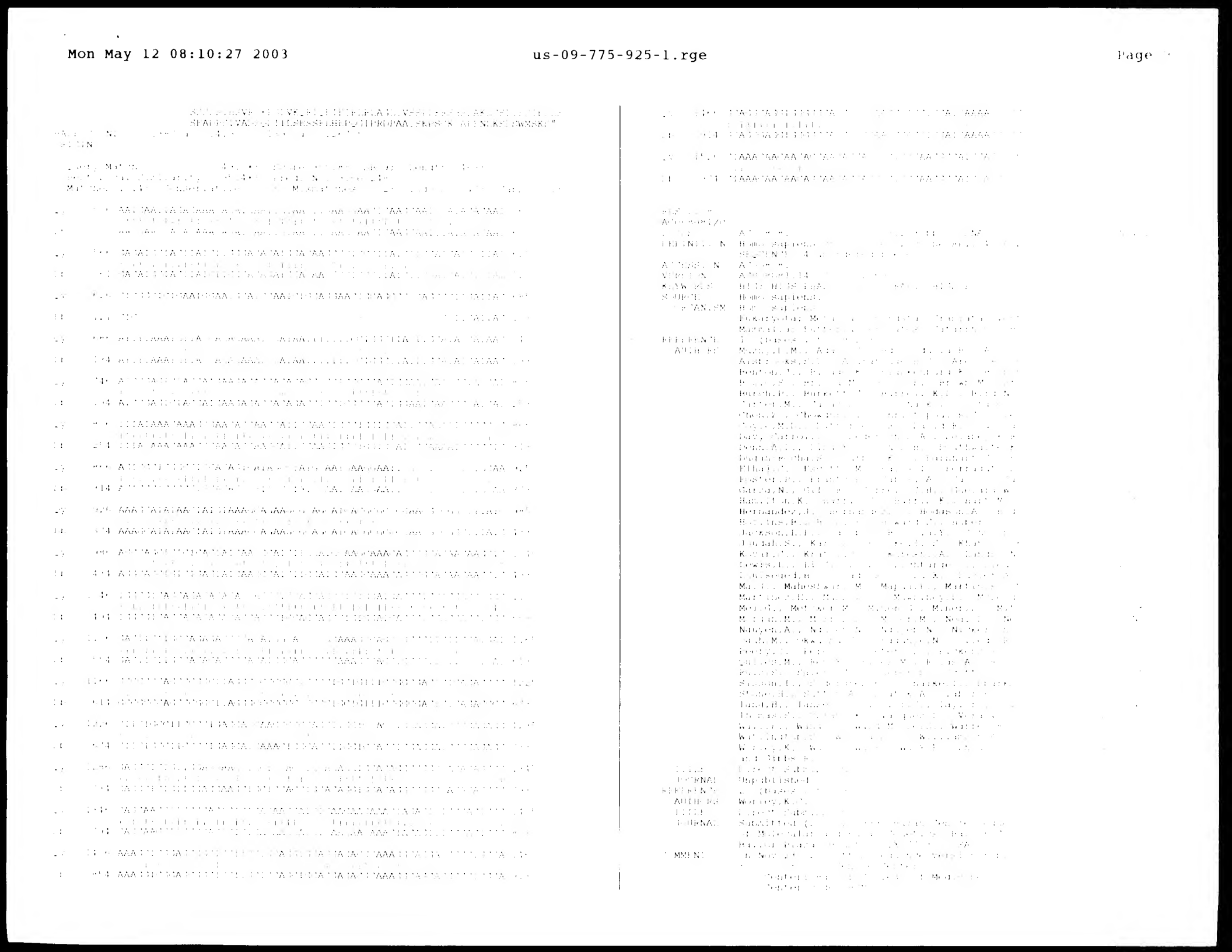

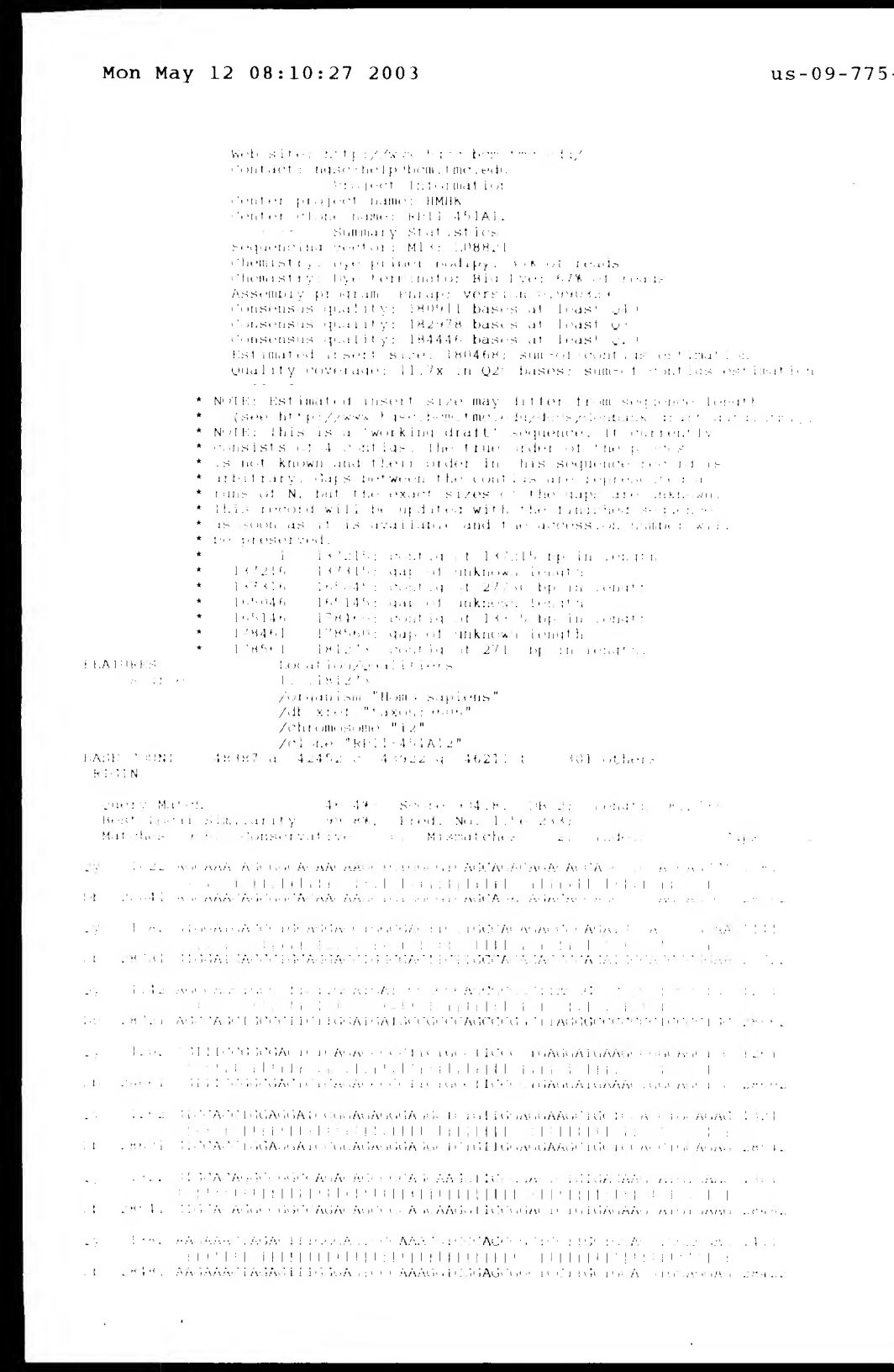

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            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible] FEB [illegible]) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX [illegible], USA
REFERENCE   3  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible] MAY [illegible]) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX [illegible], USA
COMMENT     On Apr 28, [illegible] this sequence version replaced [illegible].
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                 Contact: hgsc-help@bcm.tmc.edu
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                 Center project name: HCHH
                 Center clone name: RP11-[illegible]
                            Summary Statistics
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                 Chemistry: Dye-terminator [illegible]
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                 Quality coverage: [illegible] bases; sum [illegible]

          * NOTE: Estimated insert size may differ from sequence length
          *   (see http://[illegible])
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of [illegible] contigs. The true order of the pieces
          * is not known and their order in this sequence record is
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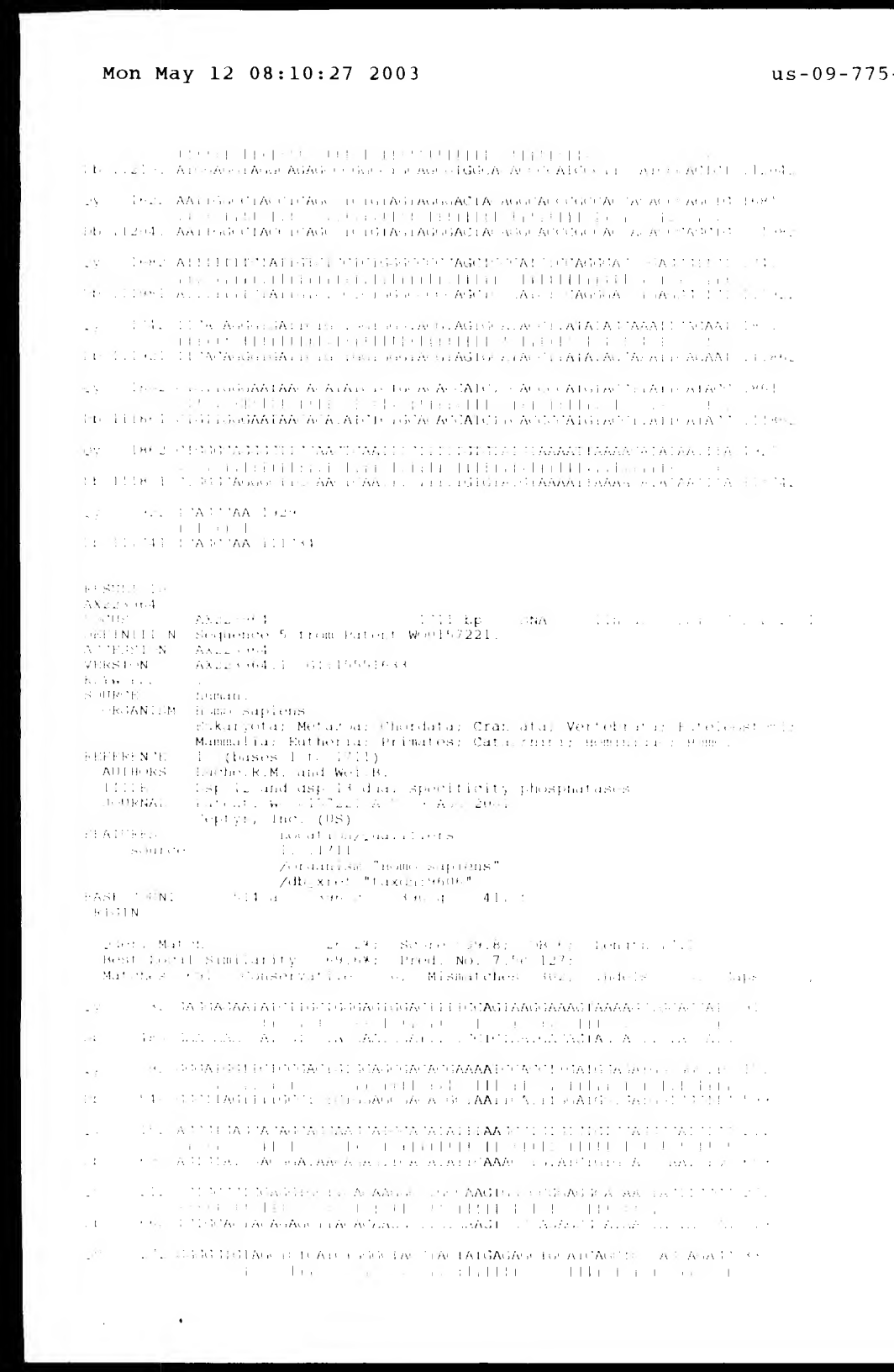

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ACCESSION AX223004
VERSION AX223004.1 GI:15553633
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2711)
AUTHORS Escher,R.M. and Wei,B.
TITLE Dsp 12 and dsp 13 dna, specificity phosphatases
JOURNAL Patent: WO 0157221-A 2 02-AUG-2001;
Syntex, Inc. (US)
FEATURES Location/Qualifiers
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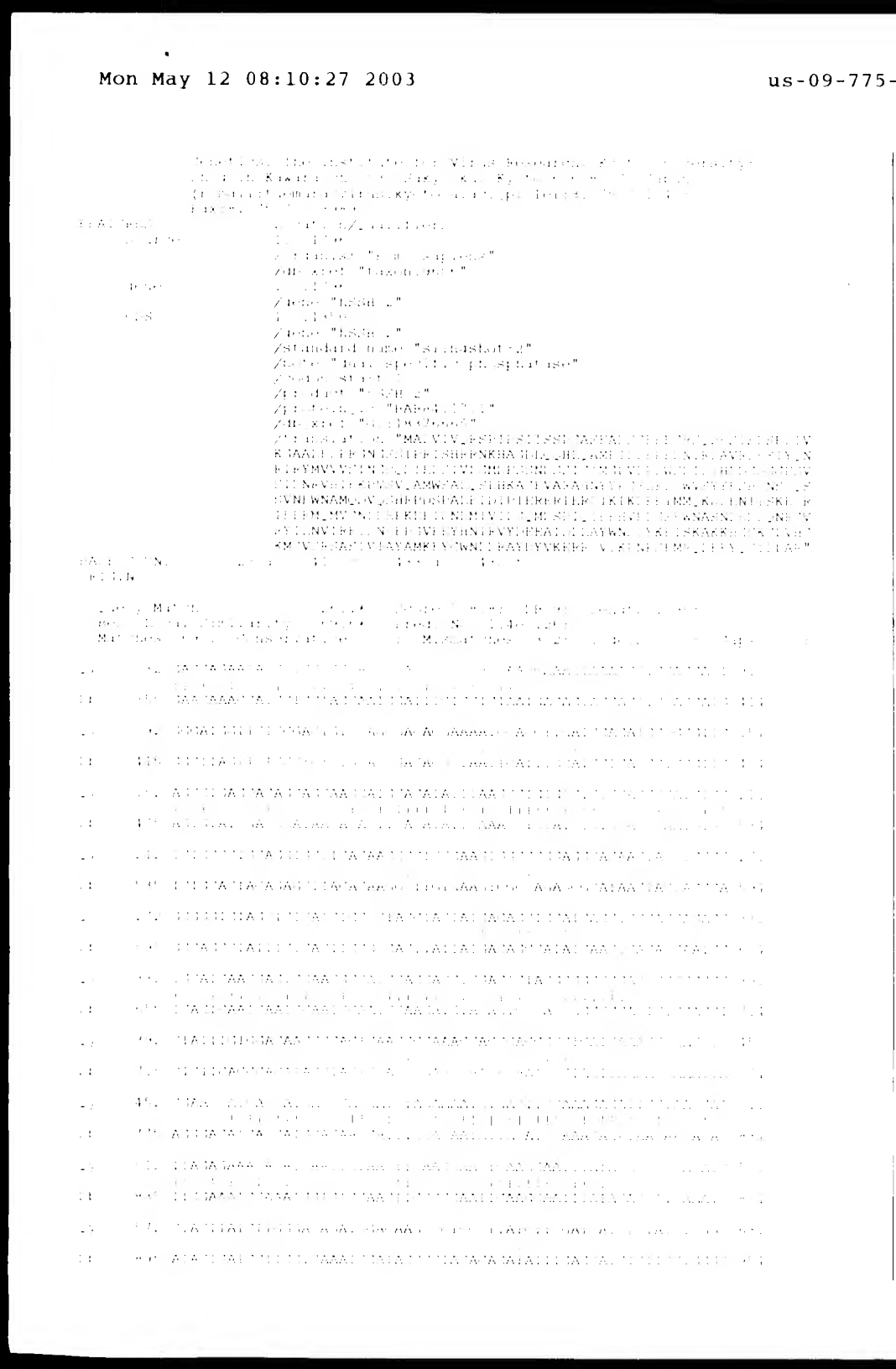
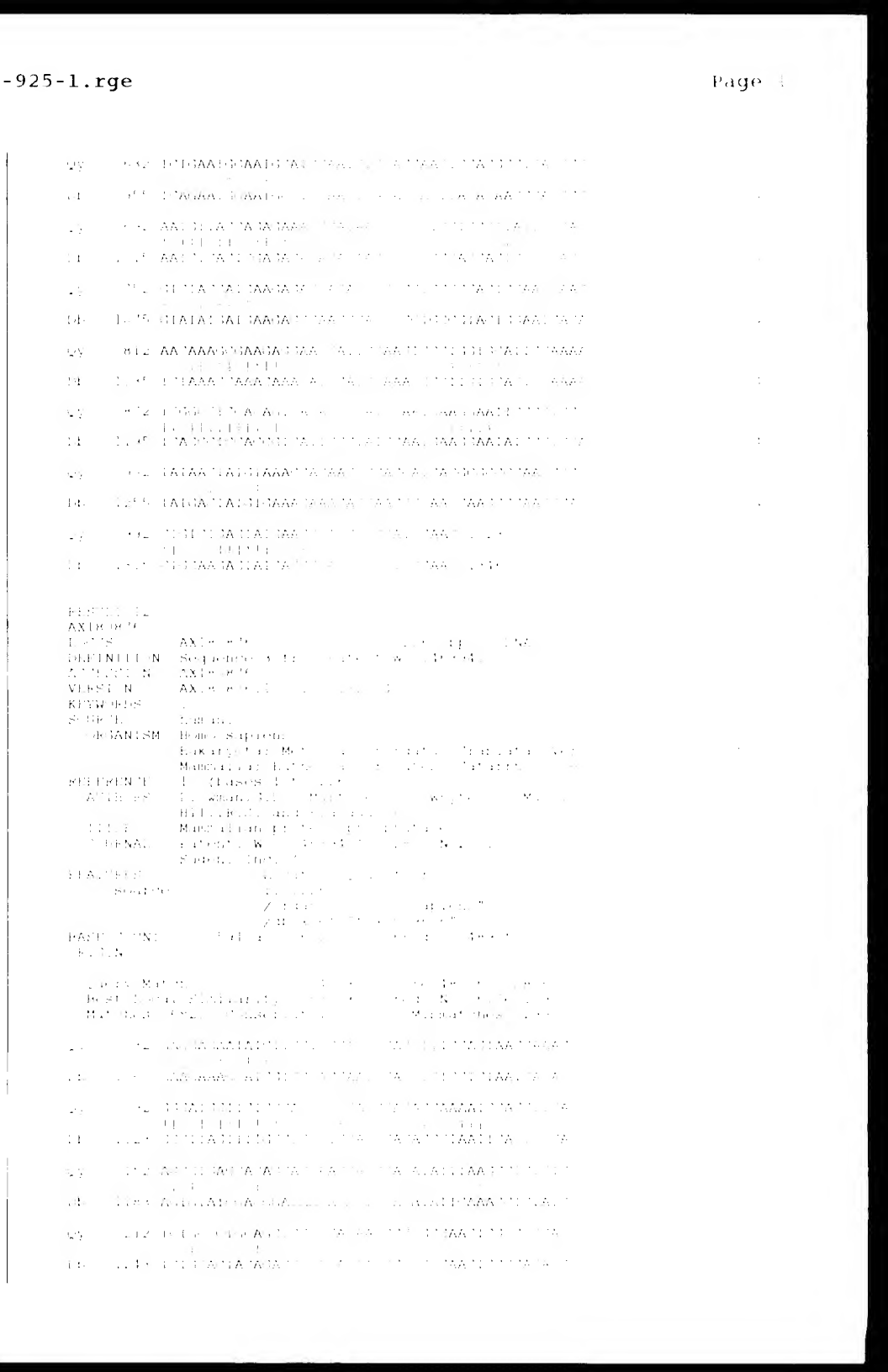
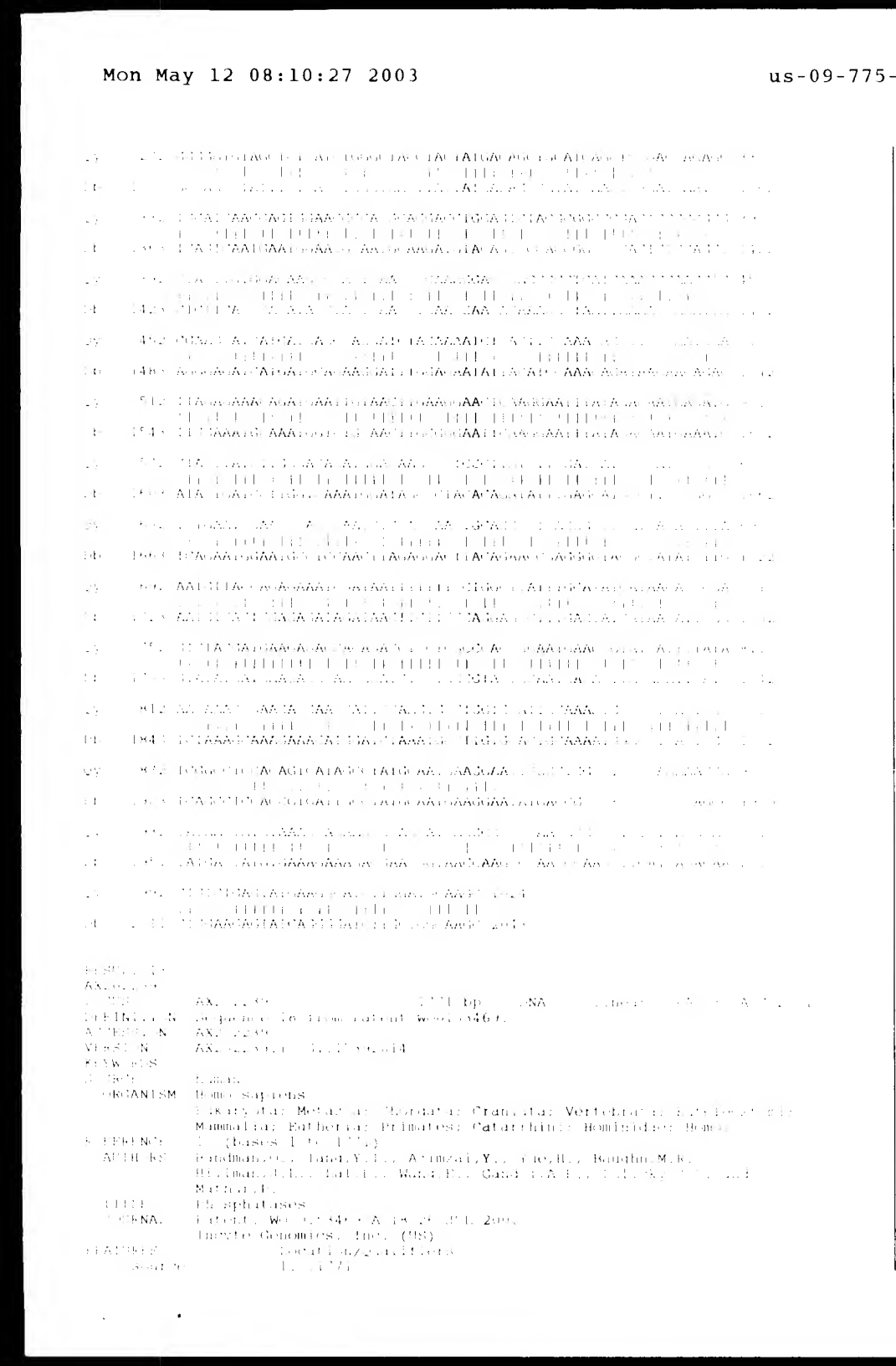
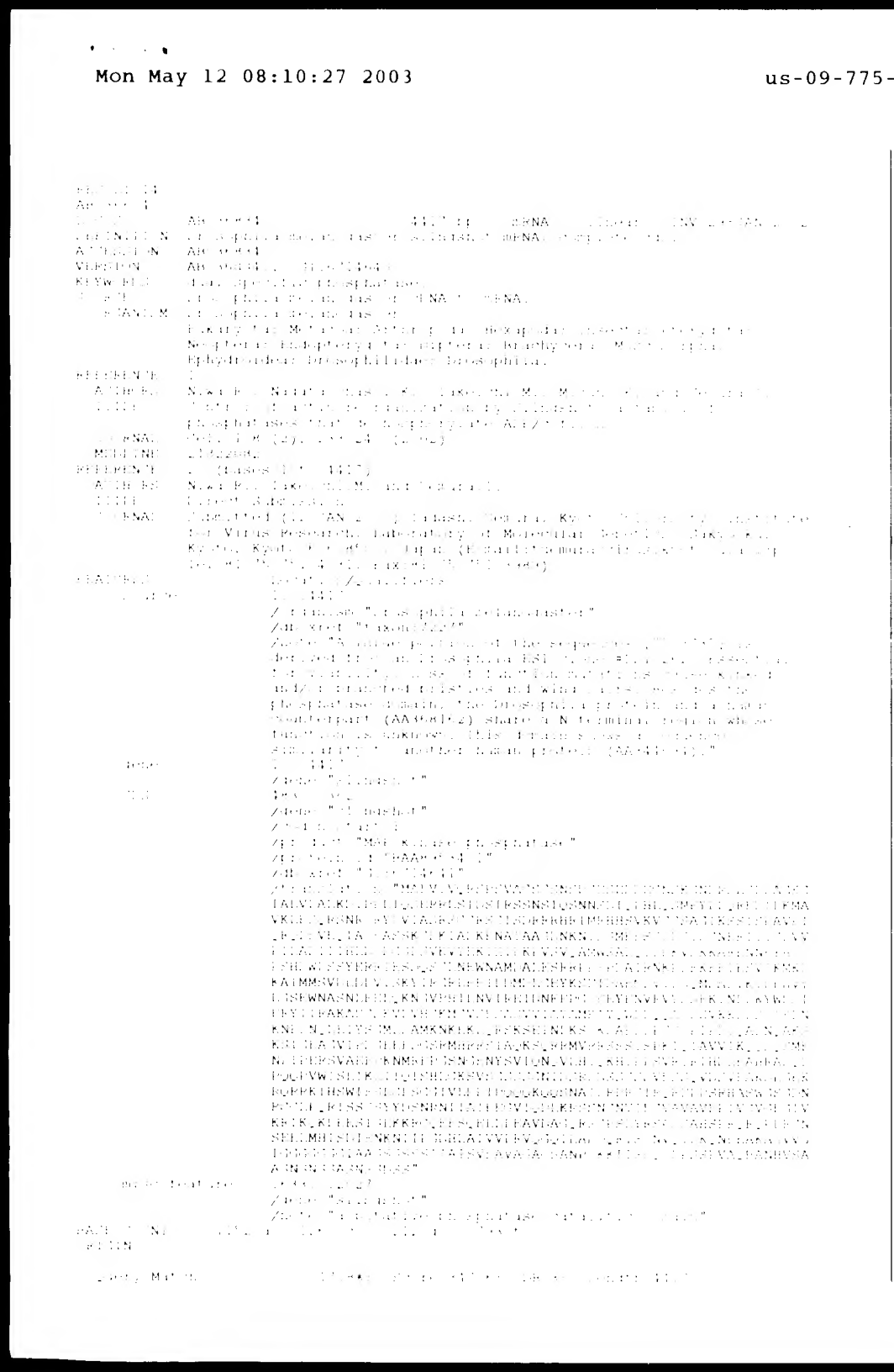
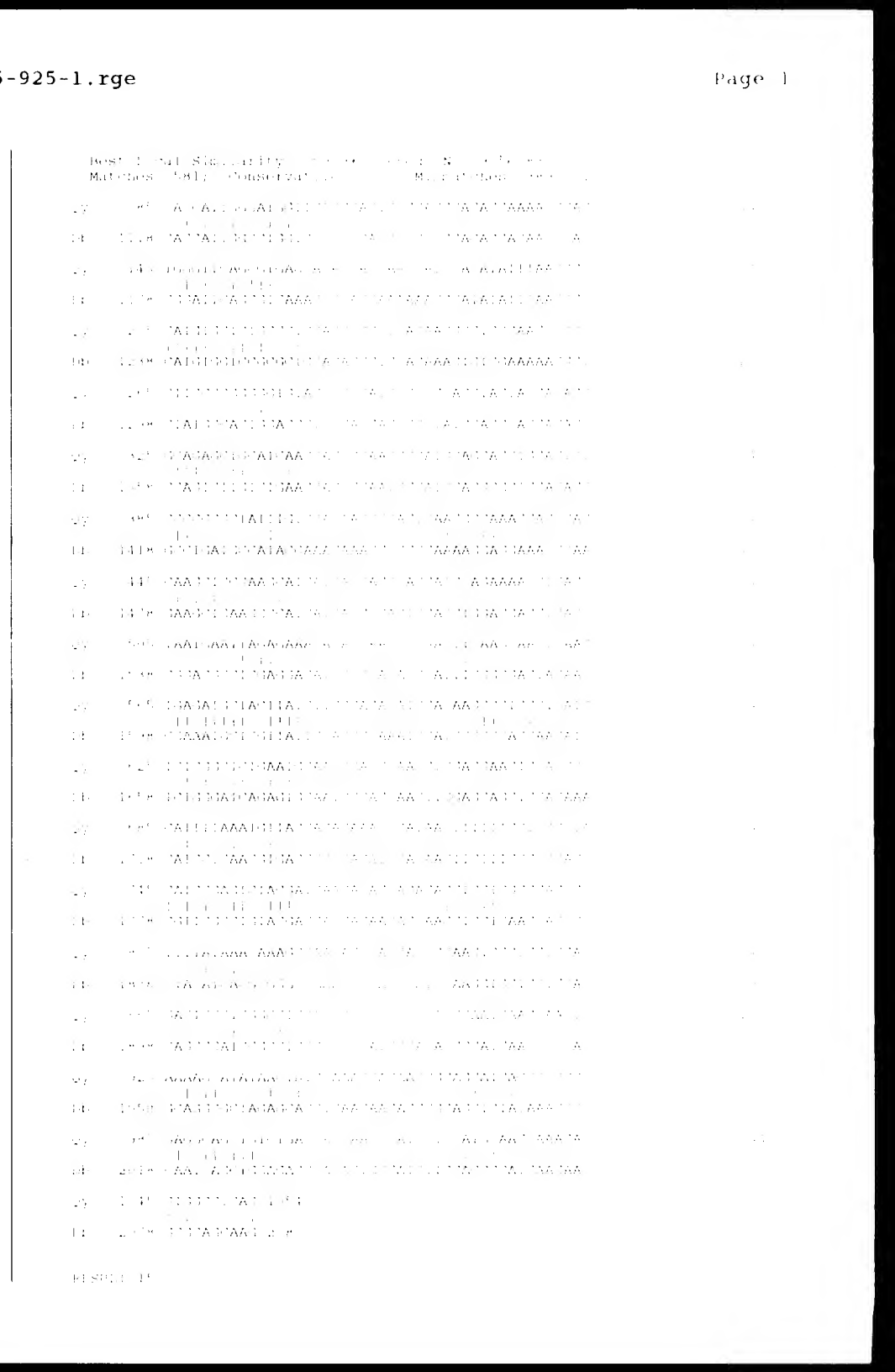
DEFINITION Homo sapiens mRNA for bSSH-2, complete cds.
ACCESSION AB072358
VERSION AB072358.1 GI:18476664
KEYWORDS .
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kinoshita,N., Nagata-Ohashi,K., Takeichi,M., Mizuno,K. and Uemura,T.
TITLE Control of actin reorganization by Slingshot, a family of phosphatases that dephosphorylate ADF/cofilin
JOURNAL Cell 109 (2), 235-245 (2002)
MEDLINE 21892984
REFERENCE 2 (bases 1 to 1796)
AUTHORS Kinoshita,N., Nagata-Ohashi,K., Takeichi,M., Mizuno,K. and Uemura,T.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-2001) Tadashi Uemura, Laboratory of Molecular

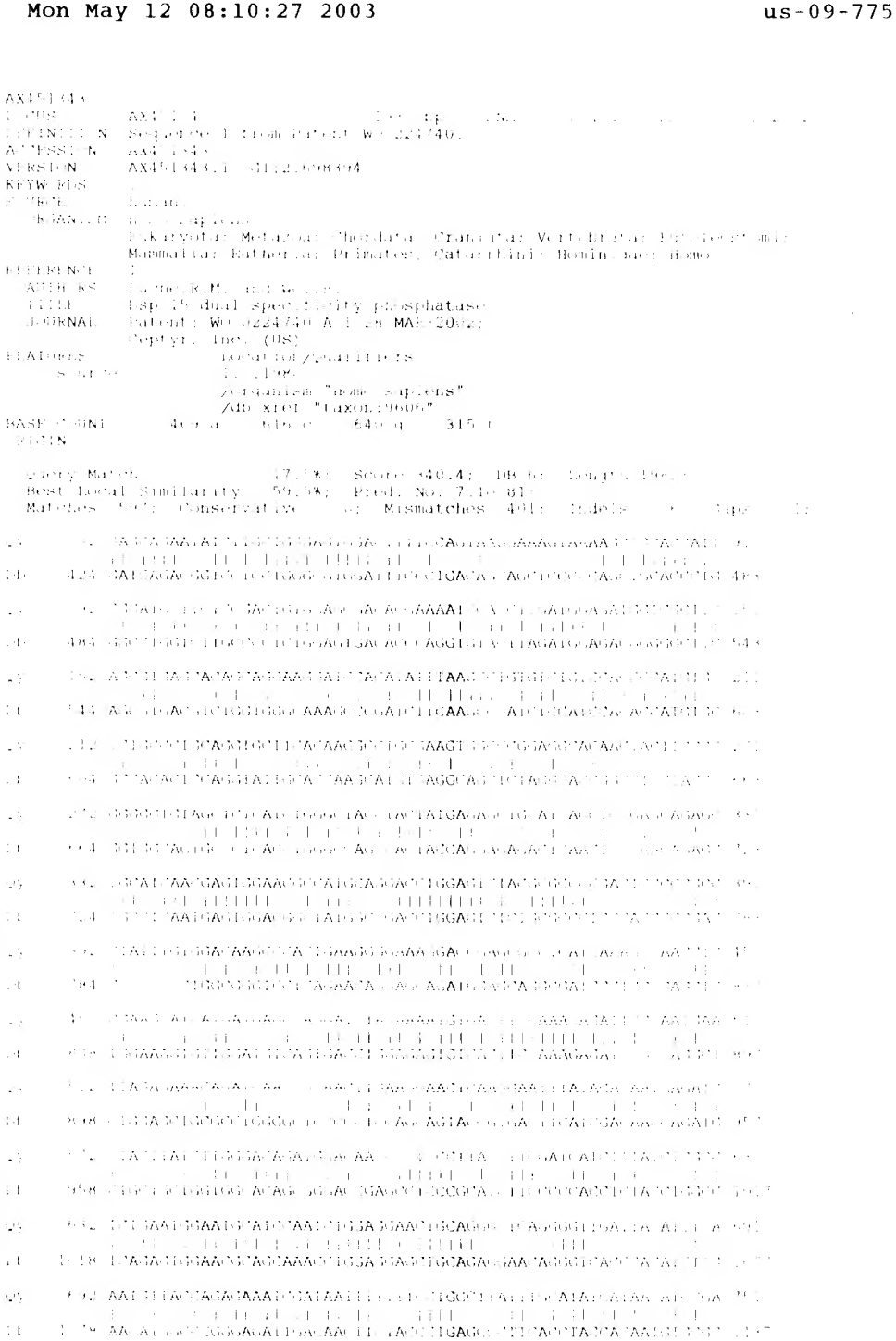












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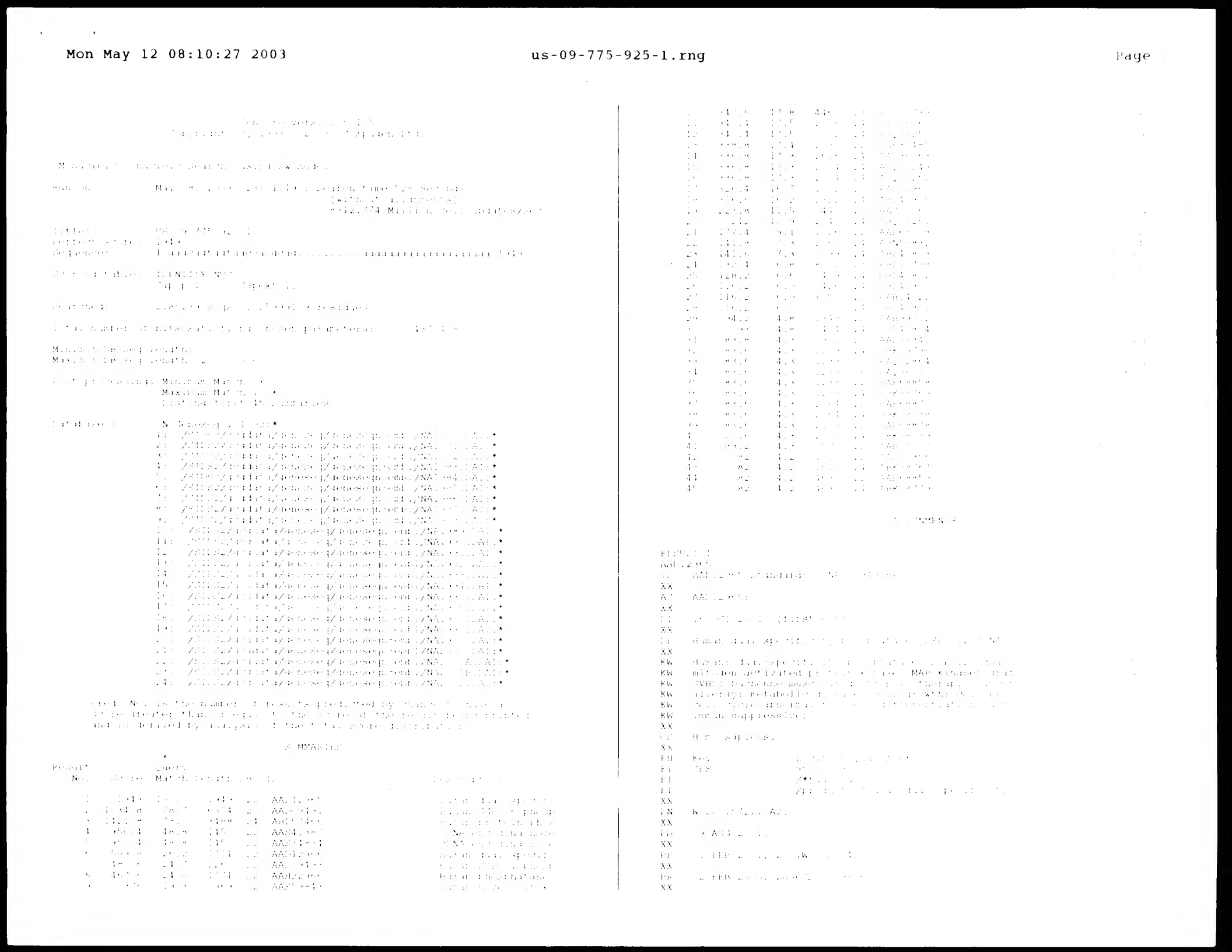

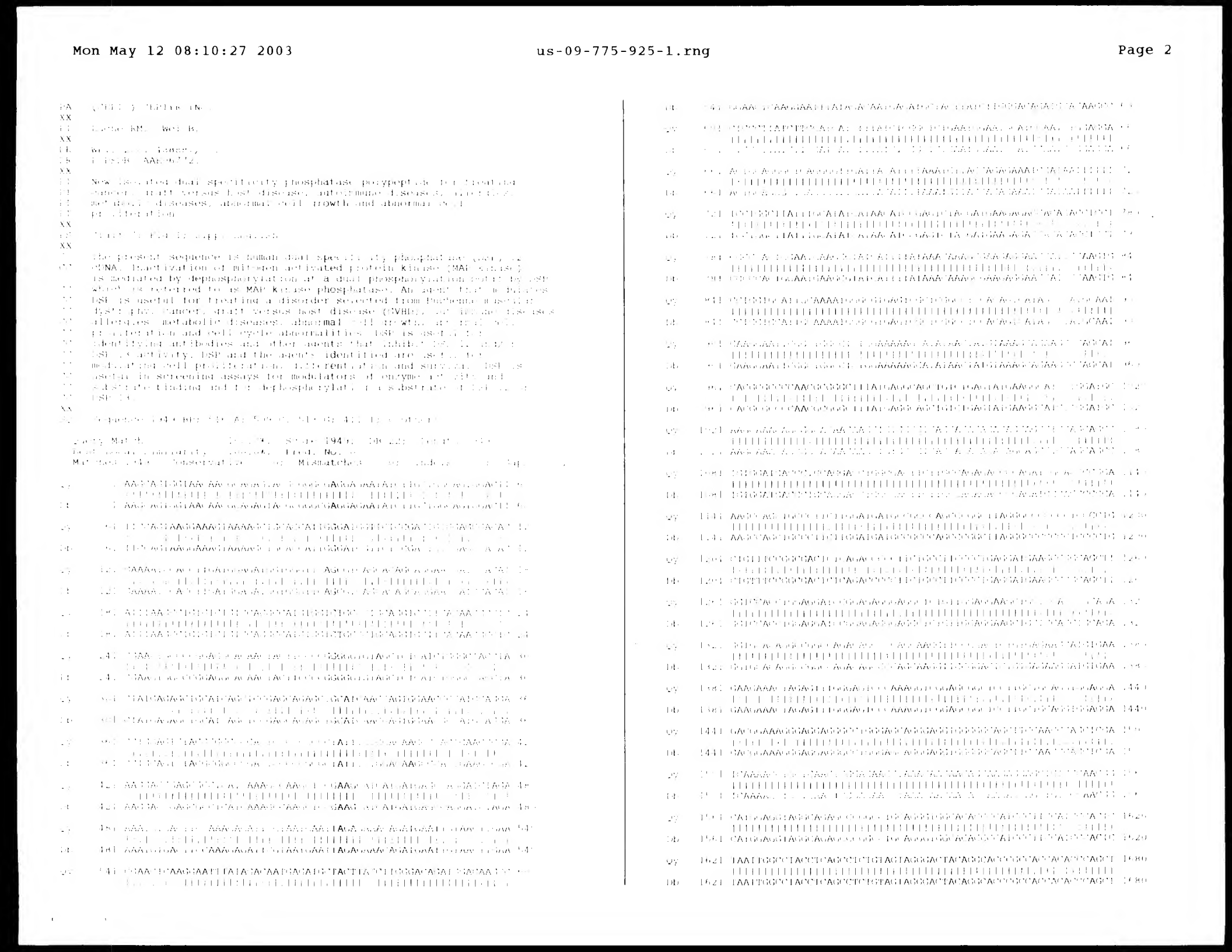

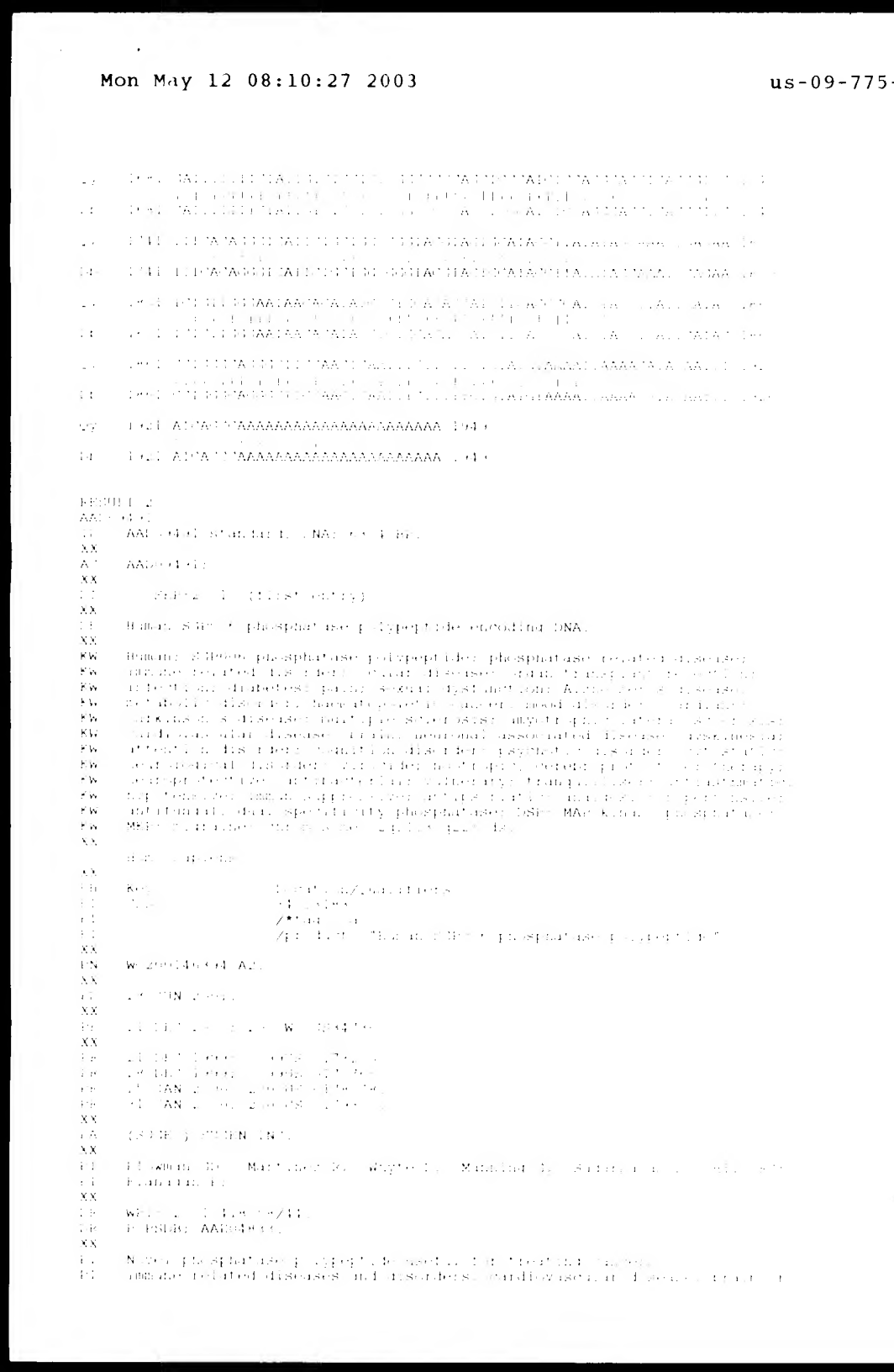

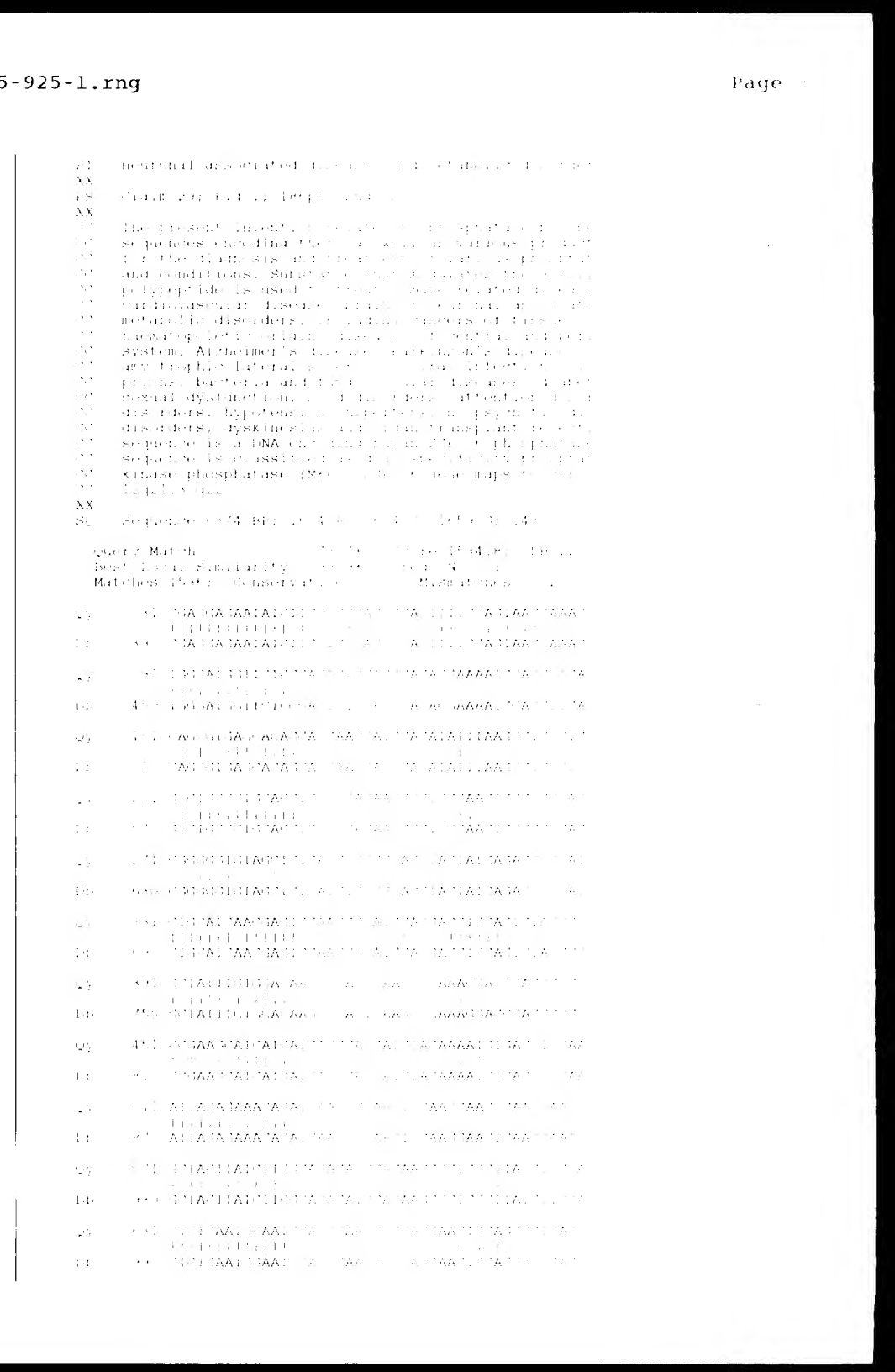

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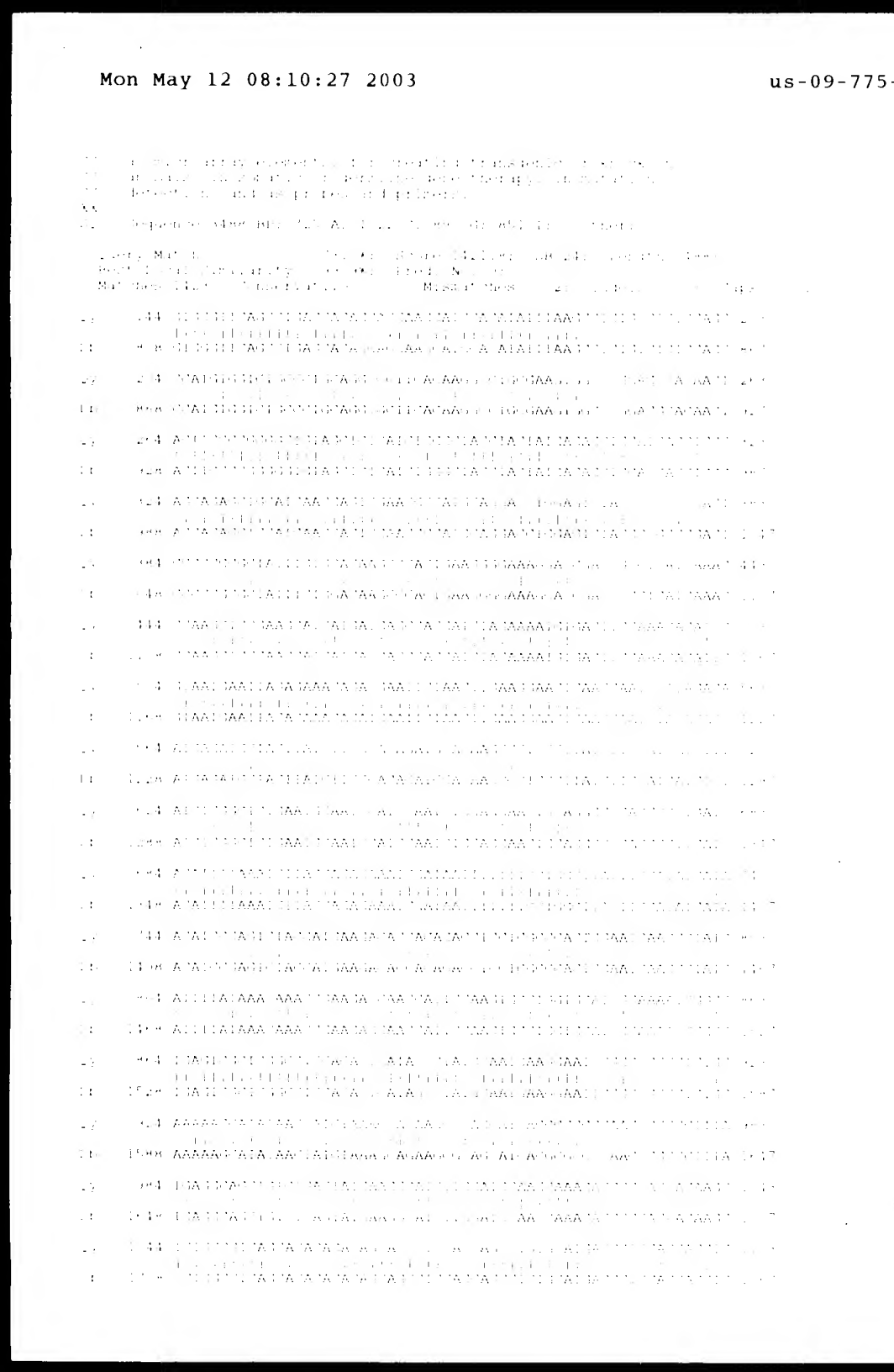
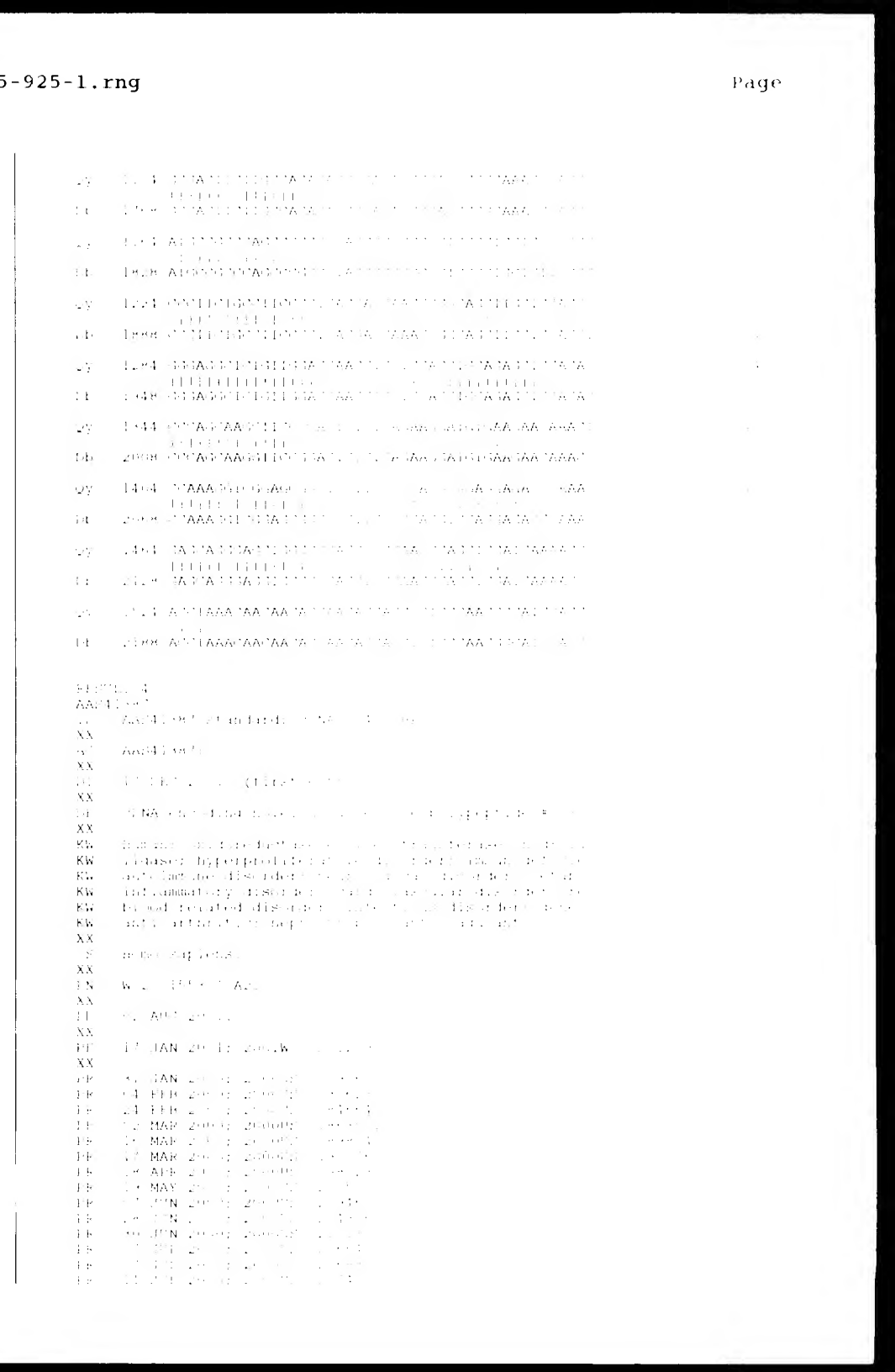
PA (INCY) INCYTE GENOMICS INC.
XX
PI Lal P, Yao MG, Walia NK, Elliott VS, Pankaj ?, Li Y;
PI Arvizo C, Bandhu MK, Yao G, Lu AM, Elbaum CM;
PI Thornton M, Gandhi AP, Lee EA, Xu Y, Wang YF, Hatzis A?A;
PI Hunkapiller K, Patterson SE, Lal P, Swarnakar A;
XX
DR WPI; 2002-404109/43.
DR P-PSDB; AB076314.
XX
PT Novel human protein phosphatase polypeptide, useful in diagnosis,
PT prevention and treatment of immune disorders such as AIDS, cancer, viral
PT disorders such as epilepsy, and developmental and neurodegenerative
PT disorders -
XX
PS Claim 5; Page 127-128; 192pp; English.
XX
CC The present sequence is the nucleotide sequence of Incyte ID
CC 5129906CB1 encoding a novel protein phosphatase, designated PP 2
CC (or AB076314). Putative protein phosphatases were initially
CC identified by running the Genscan gene identification program
CC against public genomic sequence databases. When necessary, the
CC predicted sequences were then edited to correct errors such as
CC extra or omitted exons. Full length polynucleotide sequences were
CC obtained by assembling predicted coding sequences with Incyte cDNA
CC sequences and/or partial cDNA sequences, or were derived directly
CC from edited or unedited Genscan predicted coding sequences. The
CC present sequence includes sequences obtained from several cDNA
CC libraries and from exons predicted from genomic DNA. A
CC representative library for the full length sequence is CORPNOT1.
CC The encoded protein shows 97% identity to Drosophila MAP kinase
CC phosphatase and contains a dual specificity phosphatase catalytic
CC domain. The invention provides protein phosphatase PP 2, PP 2
CC nucleic acids and polypeptides, expression vectors, host cells,
CC antibodies, agonists and antagonists. These are useful in the
CC diagnosis, treatment and prevention of disorders associated with
CC aberrant expression of protein phosphatase, including an immune
CC system disorder (e.g. AIDS, Addison's disease, allergy, asthma,
CC atherosclerosis, multiple sclerosis, psoriasis), a neurological
CC disorder (e.g. Alzheimer's disease, Parkinson's disease, dementia,
CC depression, epilepsy, Tourette's disorder), developmental disorder
CC (e.g. renal tubular acidosis, myelodysplastic syndrome), an
CC proliferative disorder (e.g. arteriosclerosis, cirrhosis,
CC hepatitis) including cancer. The nucleic acids are also useful





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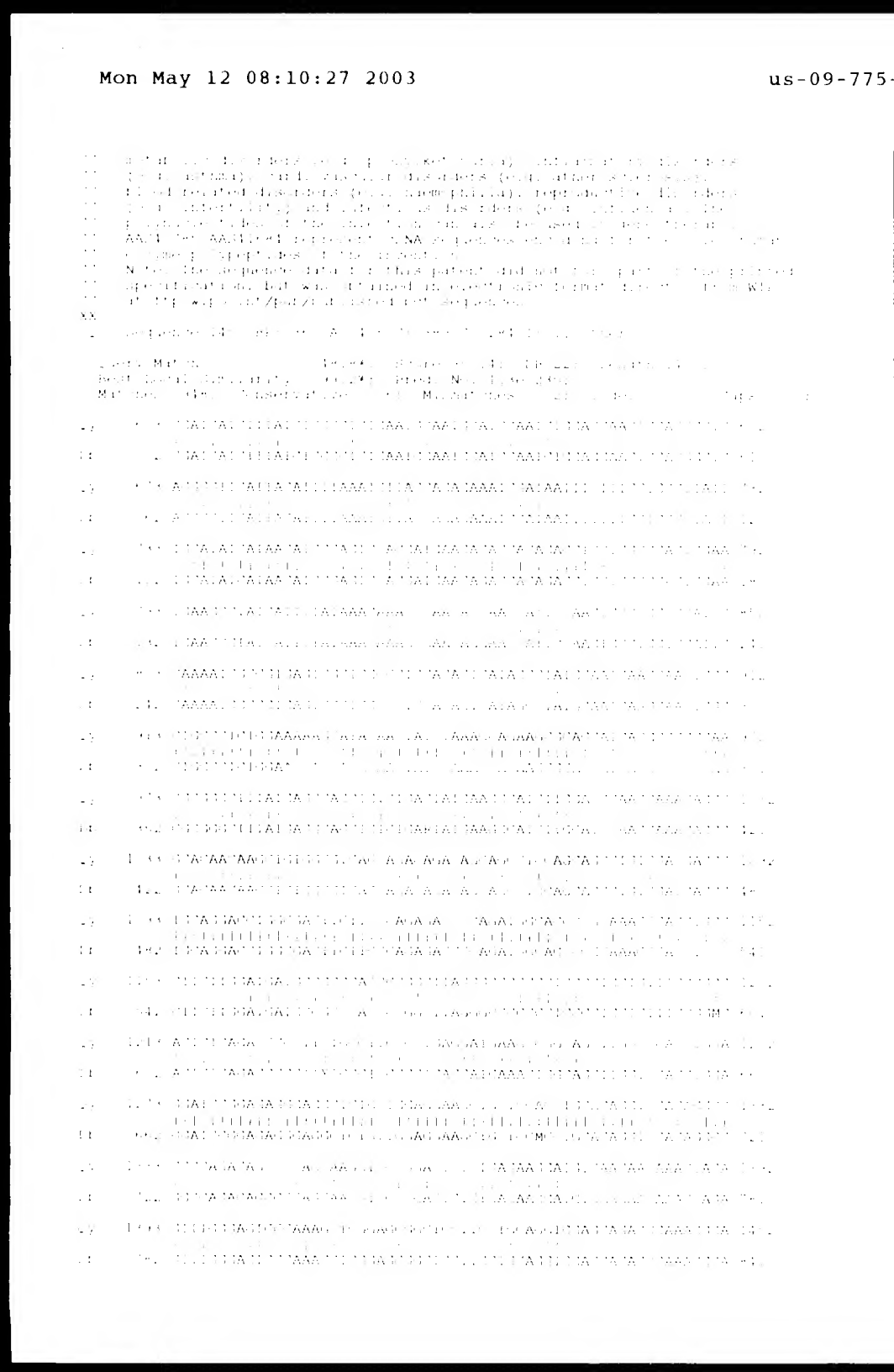
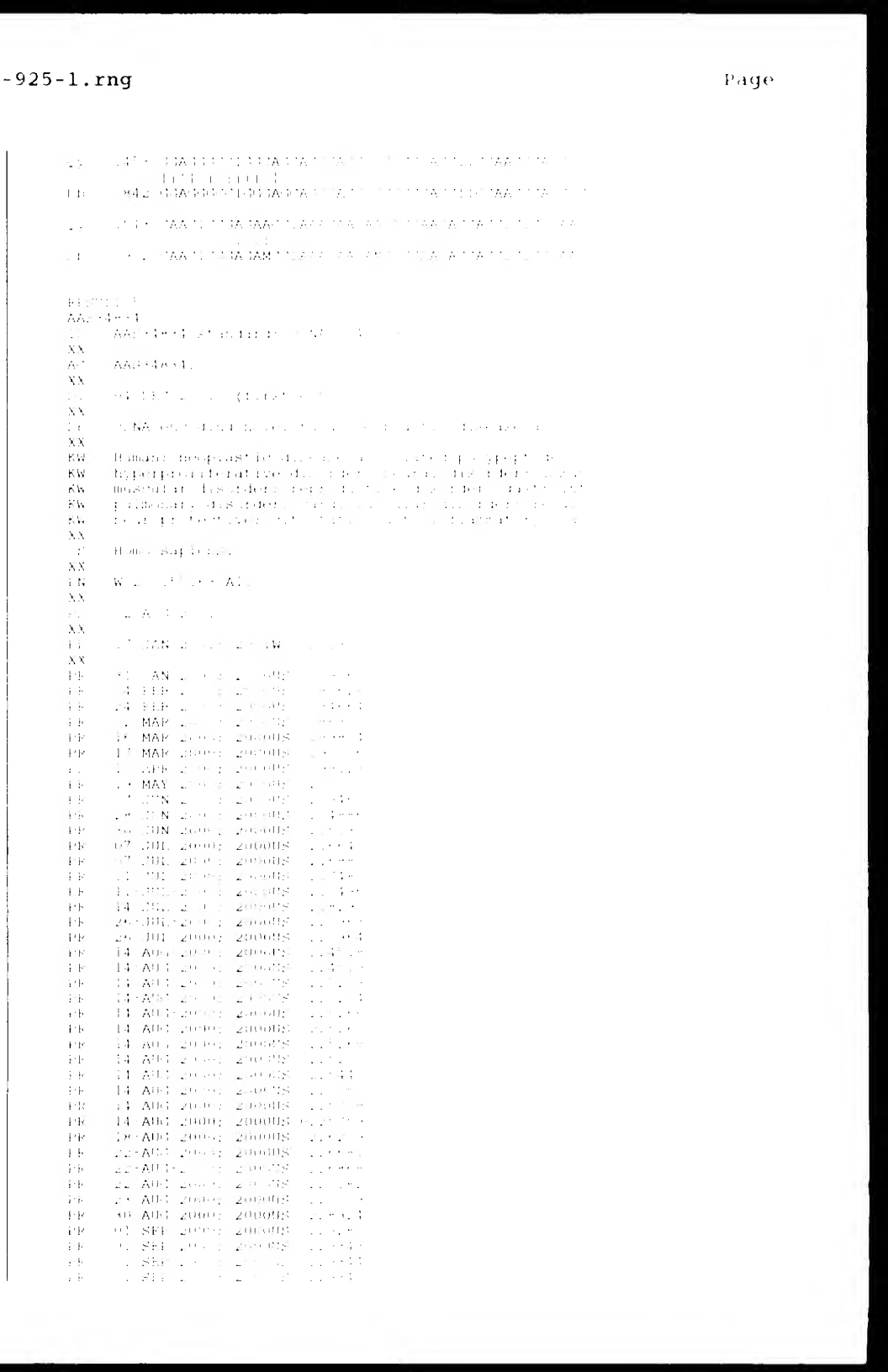
PR 11 DEC 2000; 20000US 0254097.
PR 05 JAN 2001; 20001US 0259078.
XX
PA (HUMA) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
DR P-PSDB; AAU23517.
XX
PT Novel polypeptides and polynucleotides useful for diagnosis,
PT prevention, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancers
PT diseases
XX
PS Claim 4; SEQ ID NO 615; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915 AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),





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PR   06 DEC 2000; 2000US-0251479.
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PR   11 DEC 2000; 2000US-0254097.
PR   05 JAN 2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465558/50.
DR   P-PSDB; AAU21635.
XX
PT   Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT   diagnose diseases or disorders associated with aberrant expression or
PT   activity of polypeptides, and for treating cancers, rheumatoid
PT   arthritis
XX
PS   Claim 4; SEQ ID No 78; 68pp; English.
XX
CC   The present invention relates to the isolation of novel human neoplastic
CC   disease associated polypeptides (AAU21568-AAU21851), and DNA and RNA
CC   sequences encoding for these polypeptides. The sequences of the
CC   invention are useful in the diagnosis, treatment, prevention and/or
CC   prognosis of disorders involving neoplastic disease such as
CC   hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder
CC   cancer, brain stem glioma, adult liver cancer, childhood cerebellar
CC   astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may
CC   also be useful for treating other disorders such as neural disorders,
CC   immune system disorders, muscular disorders, reproductive disorders,
CC   gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
CC   and renal disorders. The polynucleotide sequences of the invention are
CC   also useful in gene therapy. AAS34767-AAS35050 represent DNA sequences
CC   encoding for the novel human neoplastic disease associated polypeptides
CC   of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1450 BP; 360 A; 406 C; 389 G; 284 T; 11 other;

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  Matches  948;  Conservative    6;  Mismatches    2;  Indels    [illegible];  Gaps    [illegible];

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||
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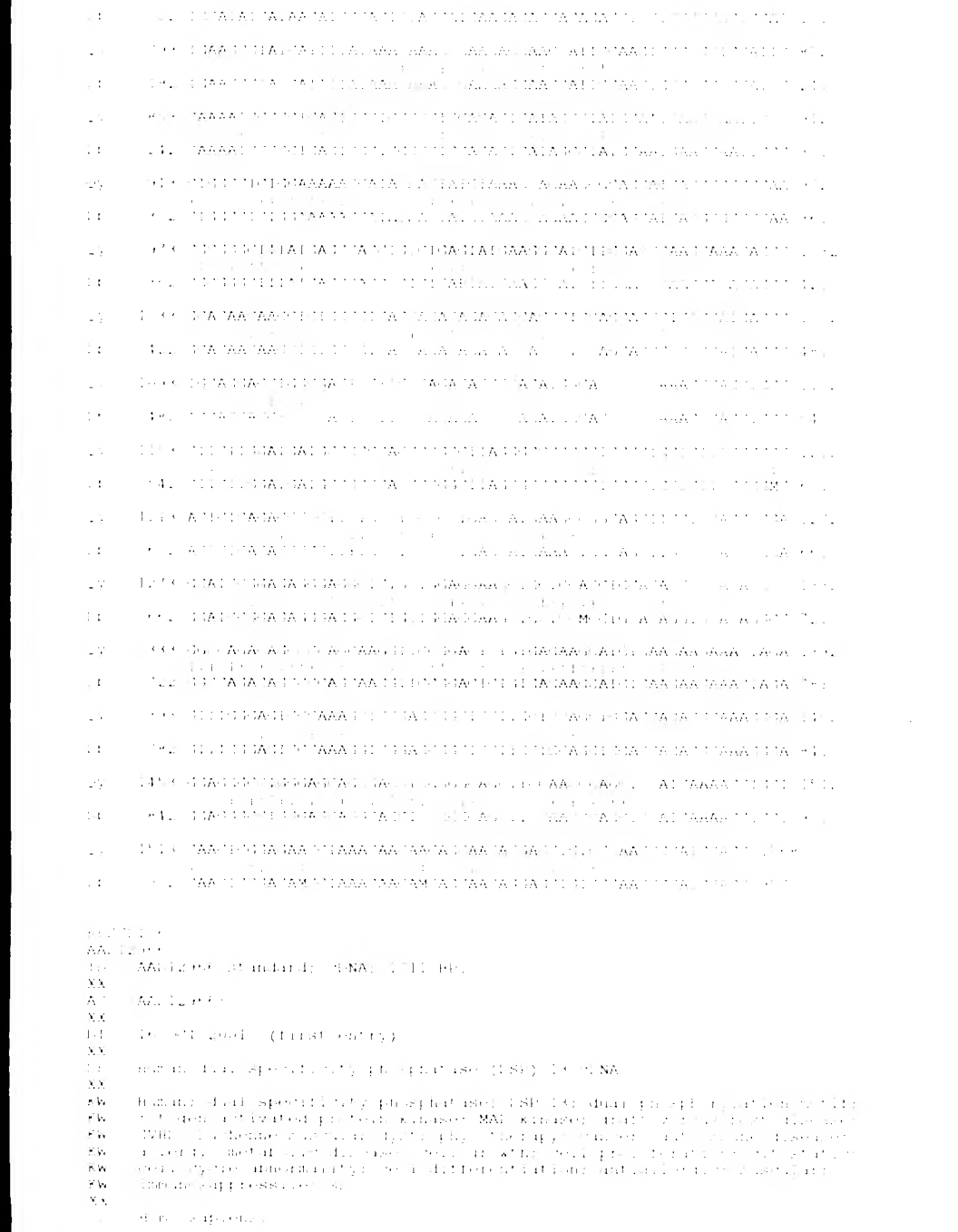

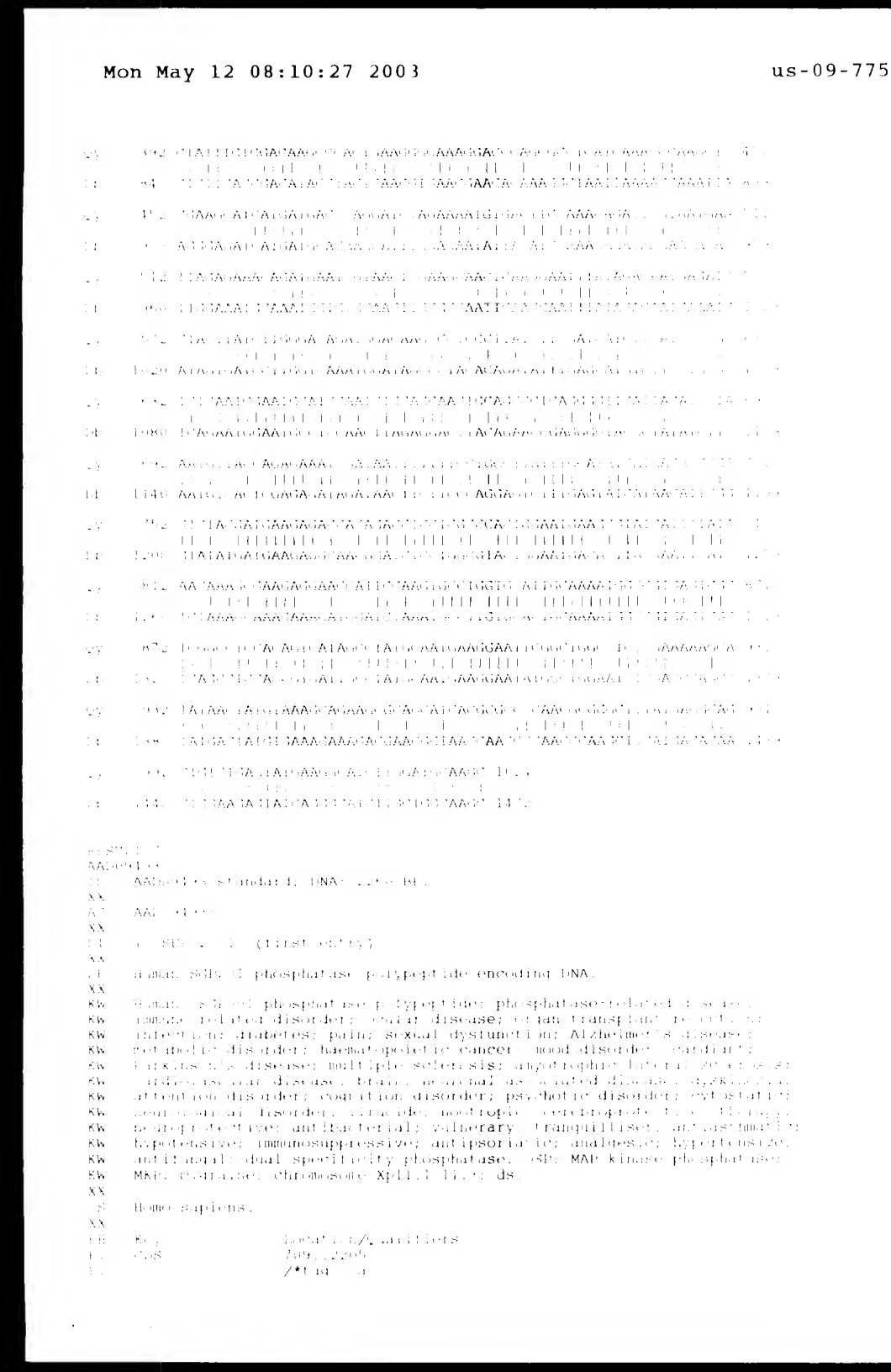

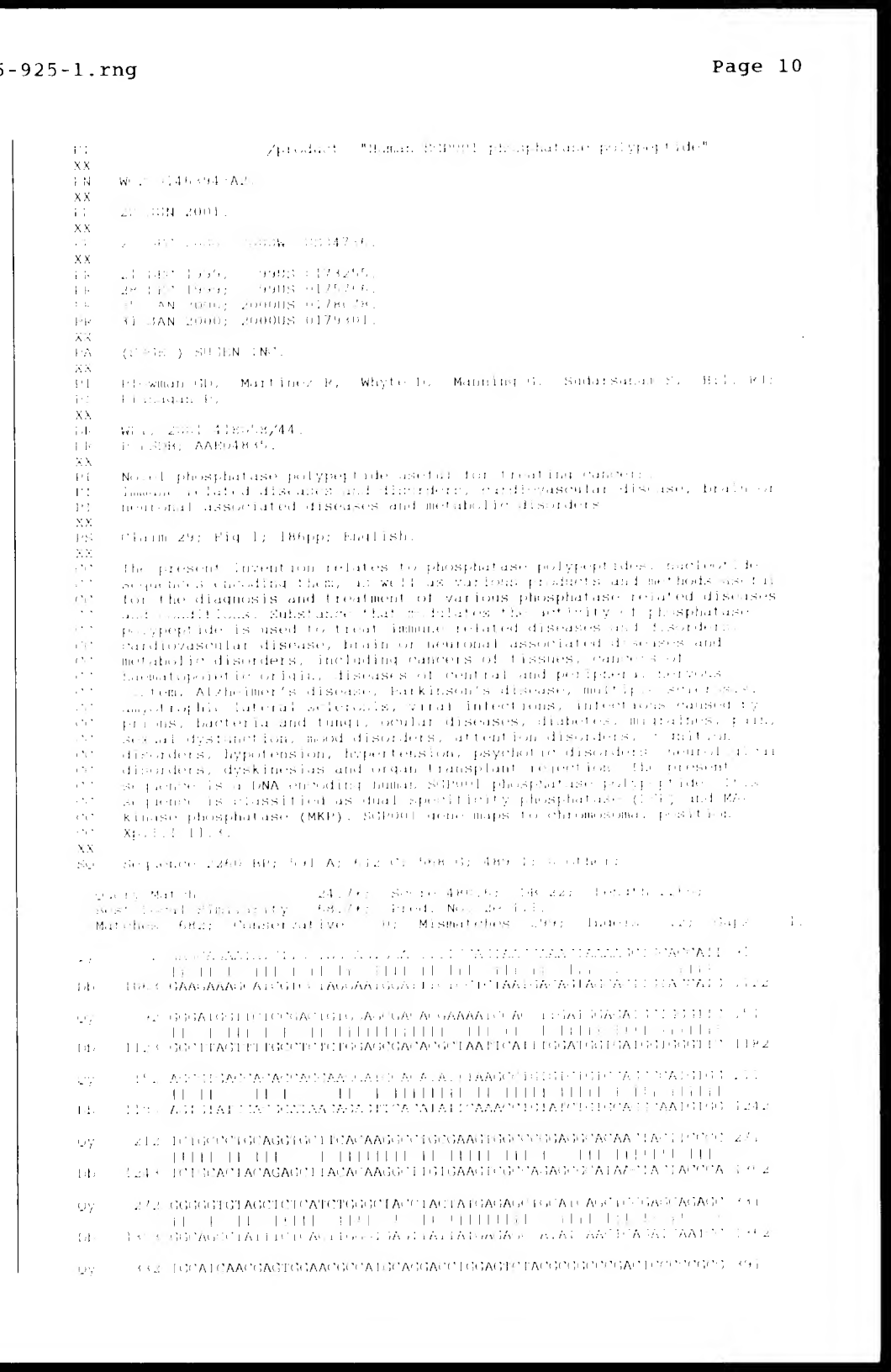

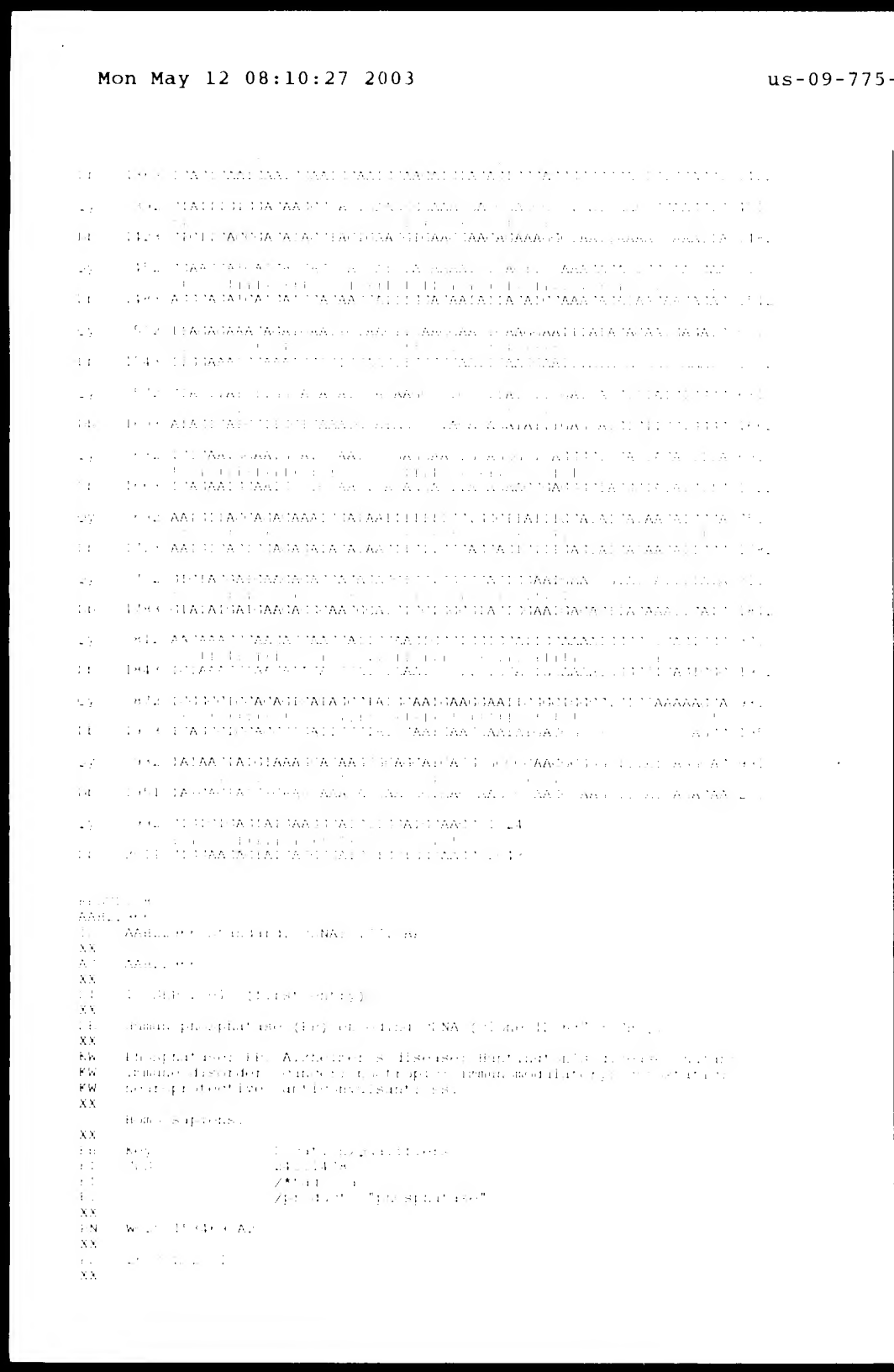

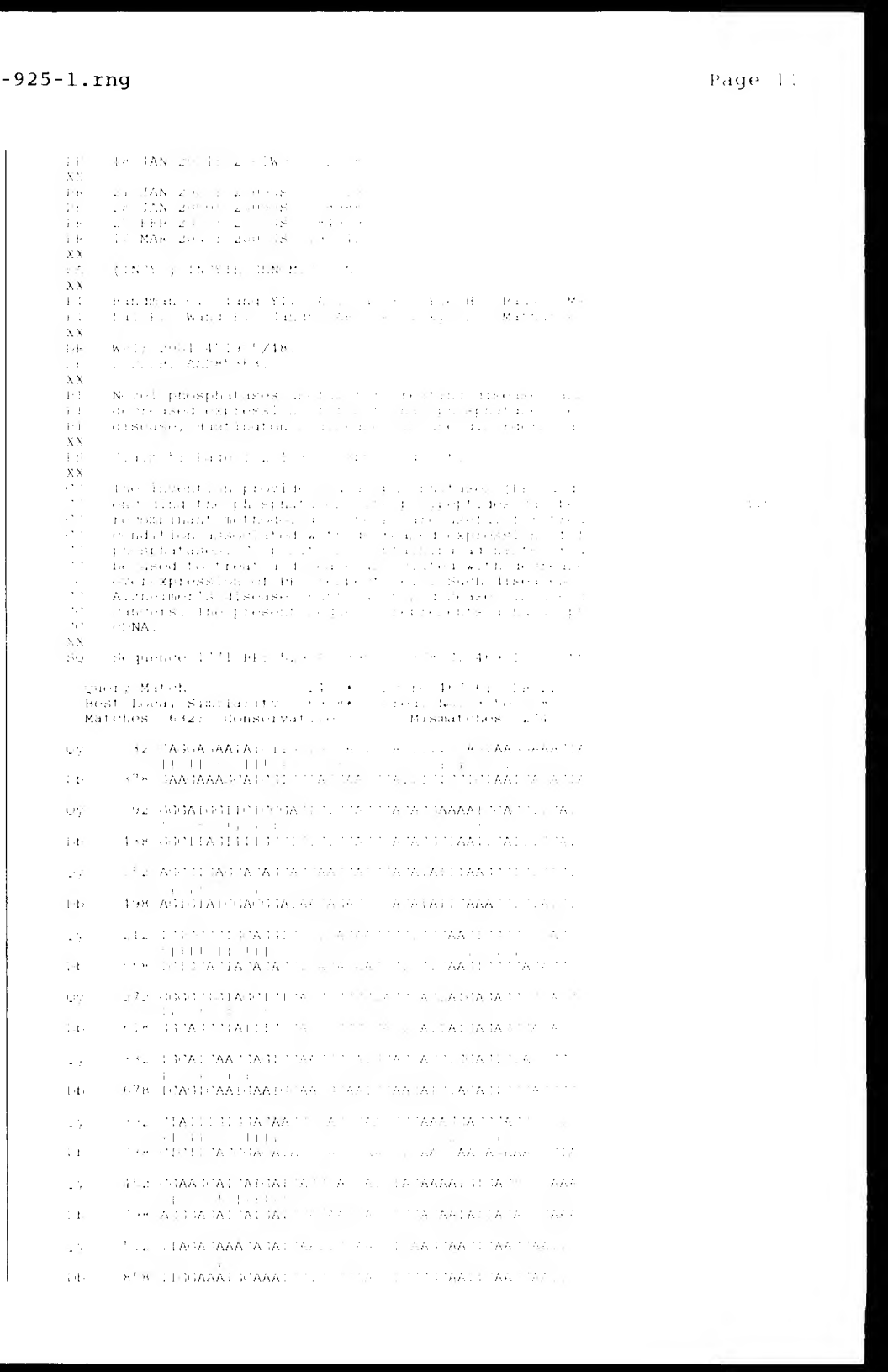

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Qy      [illegible]
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Qy      [illegible]
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Qy      [illegible]
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Qy      [illegible] TATAAT 437

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RESULT 9
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XX
AC   AAS[illegible];
XX
DT   [illegible] JAN [illegible] (first entry)
XX
DE   Human novel cytokine encoding cDNA 790CIP[illegible] 12 #1.
XX
KW   Human; ss; cytokine; cell proliferation; cell differentiation;
KW   anti-inflammatory; stem cell growth factor; activin; inhibin; cancer;
KW   nervous system disease; neuropathy; Alzheimer's disease;
KW   Parkinson's disease; Huntington's disease; spinal cord disorder;
KW   head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;
KW   platelet disorder; thrombocytopaenia; stem cell disorder;
KW   aplastic anaemia; tissue regeneration; wound healing; [illegible]
KW   osteoporosis; osteoarthritis; bone degenerative disorder;
KW   periodontal disease; fibrosis; reperfusion; immune disorder; [illegible]
KW   severe combined immunodeficiency; infection; autoimmune disorder;
KW   multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;
KW   asthma; coagulation disorder; haemophilia; sepsis; nephritis;
KW   inflammatory bowel disease; food supplement.
XX
OS   Homo sapiens.
XX
PN   W[illegible] A1.
XX
PD   [illegible]
XX
PF   [illegible] MAR [illegible]
XX
PR   [illegible] MAR [illegible] 2000US [illegible].
PR   [illegible] A[illegible] 2000US [illegible].
PR   22 SEP 2000; 2000US 0668680.
PR   [illegible] 2000US [illegible].
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PR   14 MAR [illegible] 2000US [illegible].
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   [illegible] Y[illegible], Asundi V, [illegible], Xie AJ, Ren F, Zhang J, Wang J, Xu [illegible];
PI   Yang Y, [illegible] QA, Chen [illegible], Wang [illegible], Goodrich RW, [illegible]
XX
DR   W[illegible] 20[illegible].
DR   P-PSDB; AA[illegible].
XX
PT   New polypeptides and nucleic acids, useful for diagnosis, treatment of
PT   inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone
PT   degenerative disorders, cancer and promoting wound healing
XX
PS   Claim 1; Page 219-220; 336pp; English.
XX
CC   The invention relates to isolated human polypeptides (which may be
CC   cytokines) and the polynucleotides encoding them. The protein is useful
CC   for identifying a compound which binds to it (e.g. modulators, agonists
CC   and antagonists). The polynucleotides are useful as an array, for mismatch
CC   detection. The proteins and nucleic acids are useful as nutritional
CC   sources or supplements. The protein exhibits exhibits activity relating
CC   to cytokine, cell proliferation, cell differentiation, anti-inflammatory,
CC   stem cell growth factor activity, immune stimulating or immune
CC   suppressing and activin or inhibin related activities. The proteins (and
CC   antibodies raised against them) and nucleic acids are therefore useful in
CC   the diagnosis and treatment of diseases and disorders such as cancer,
CC   central and peripheral nervous system diseases and neuropathies,
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular
CC   diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,
CC   thrombocytopaenia, stem cell disorders, aplastic anaemia, for
CC   regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC   growth, and in tissue repair, healing of burns, incisions, ulcers, for
CC   treating osteoporosis, osteoarthritis, bone degenerative disorders, or
CC   periodontal disease, lung or liver fibrosis, reperfusion injury in
CC   various tissues, various immune deficiencies and disorders, including
CC   severe combined immunodeficiency (SCID), bacterial or fungal infections,
CC   autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,
CC   diabetes mellitus, myasthenia gravis), allergic reactions and conditions
CC   such as asthma or other respiratory problems, coagulation disorders,
CC   haemophilia), septic shock, sepsis, arthritis, nephritis and inflammatory
CC   bowel disease, viral infection and are useful in altering bodily
CC   characteristics. The present sequence encodes a novel protein of the
CC   invention.
XX
SQ   Sequence 969 BP; 219 A; 290 C; 278 G; 182 T; 0 other;

  Query Match             19.3%;  Score 376;  DB 22;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-85;
  Matches  376;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      [illegible] 444

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Db      [illegible]

Qy      151 CAGGTGAGGAGAGAGGAAGAGGA[illegible]ATAA[illegible]AAGCTGTTCTGTTTATTTATGTT 21[illegible]
Db      [illegible]

Qy      211 [illegible]
Db      [illegible]

Qy      271 [illegible]
Db      63[illegible] 689

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Db      7[illegible] GTTATTTGTGGACAAG 76[illegible]
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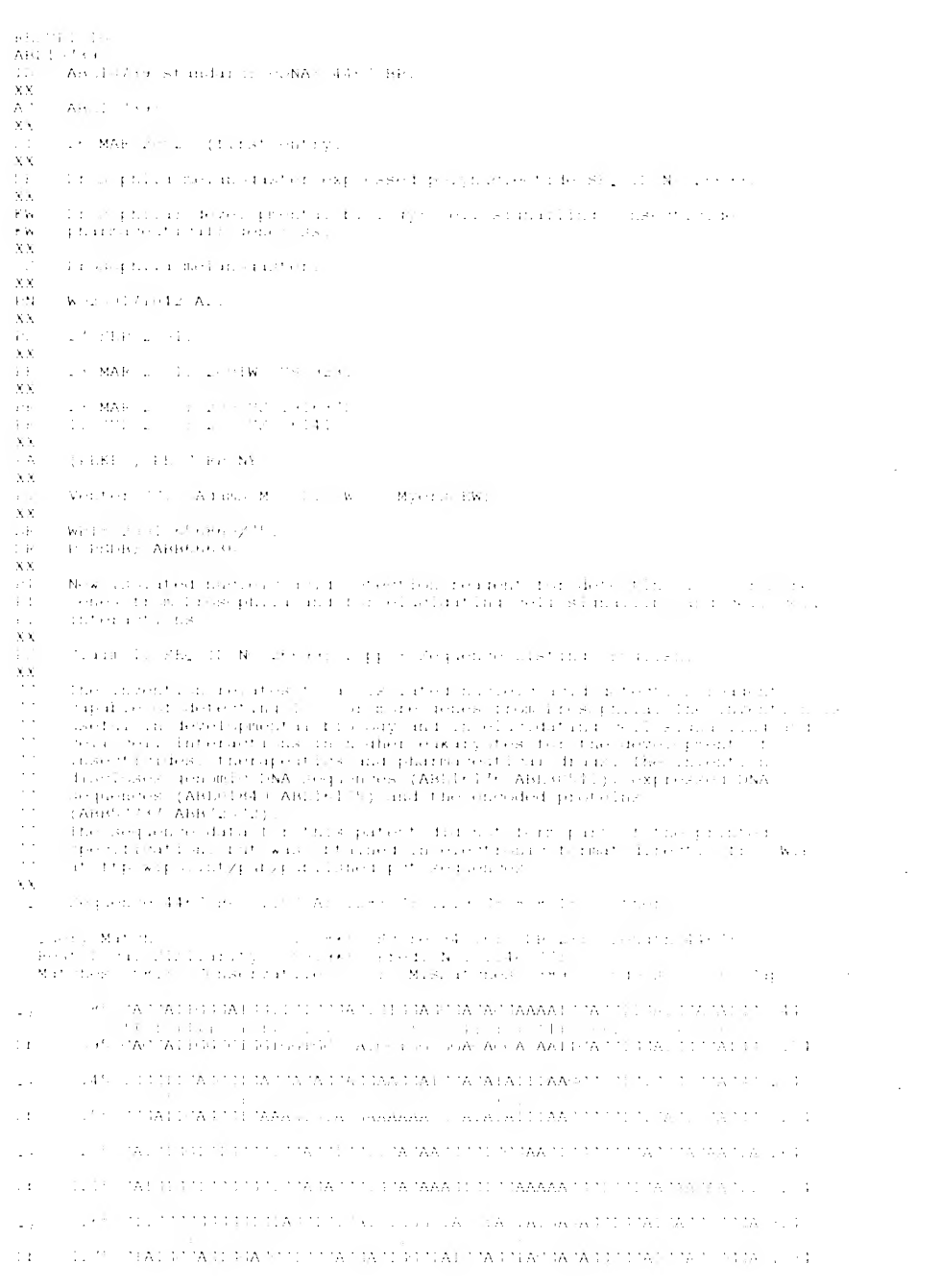
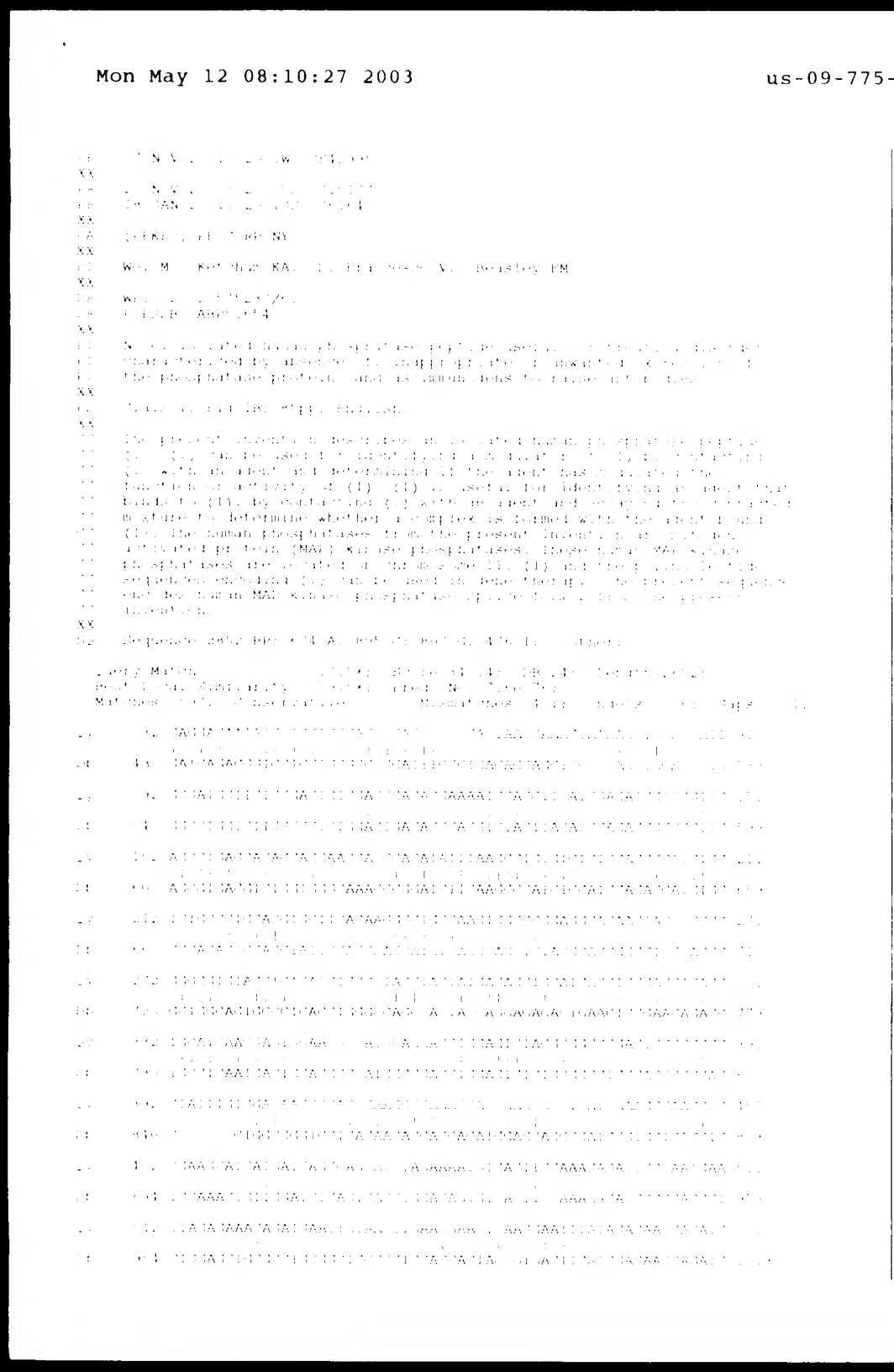
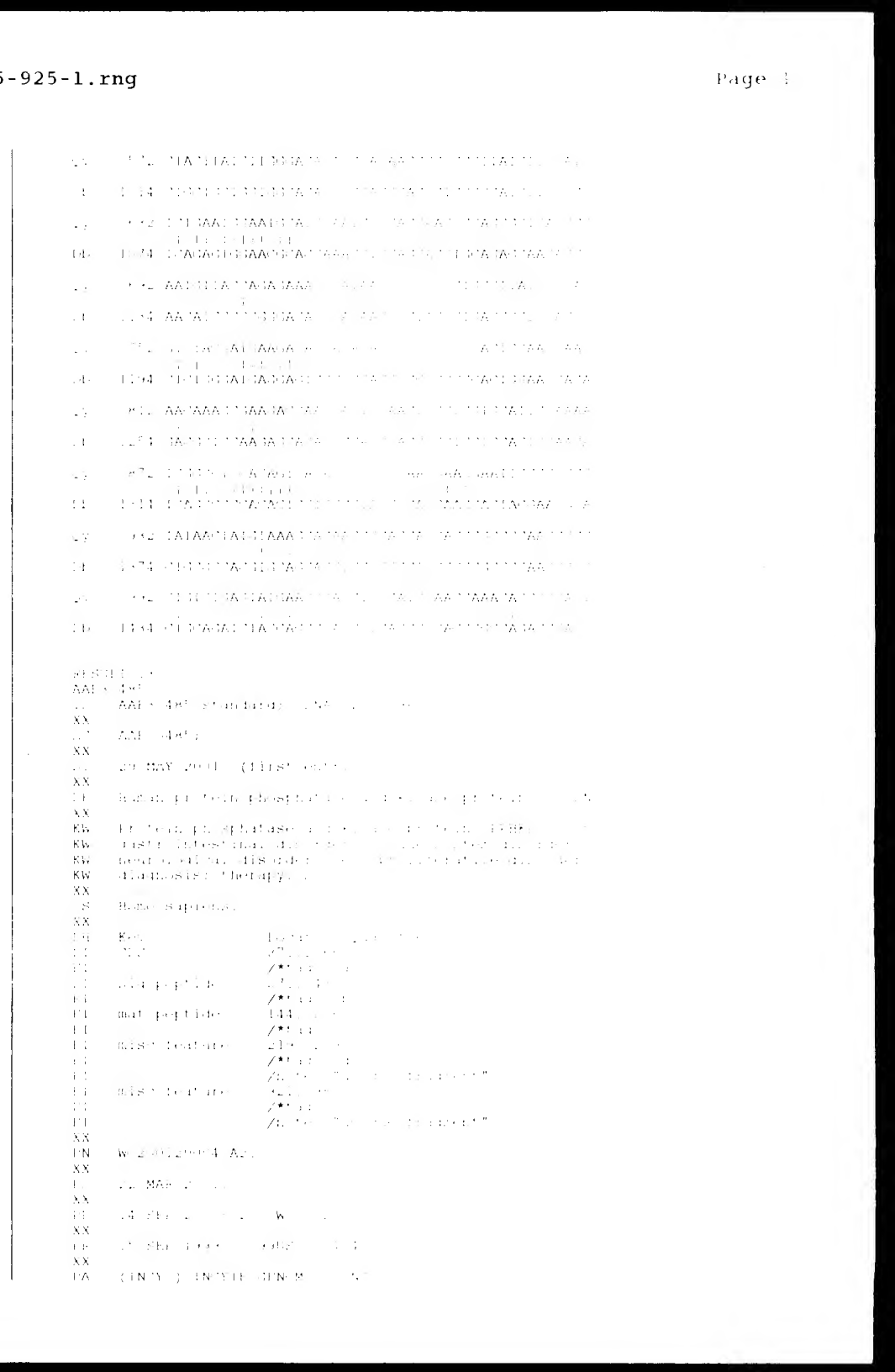
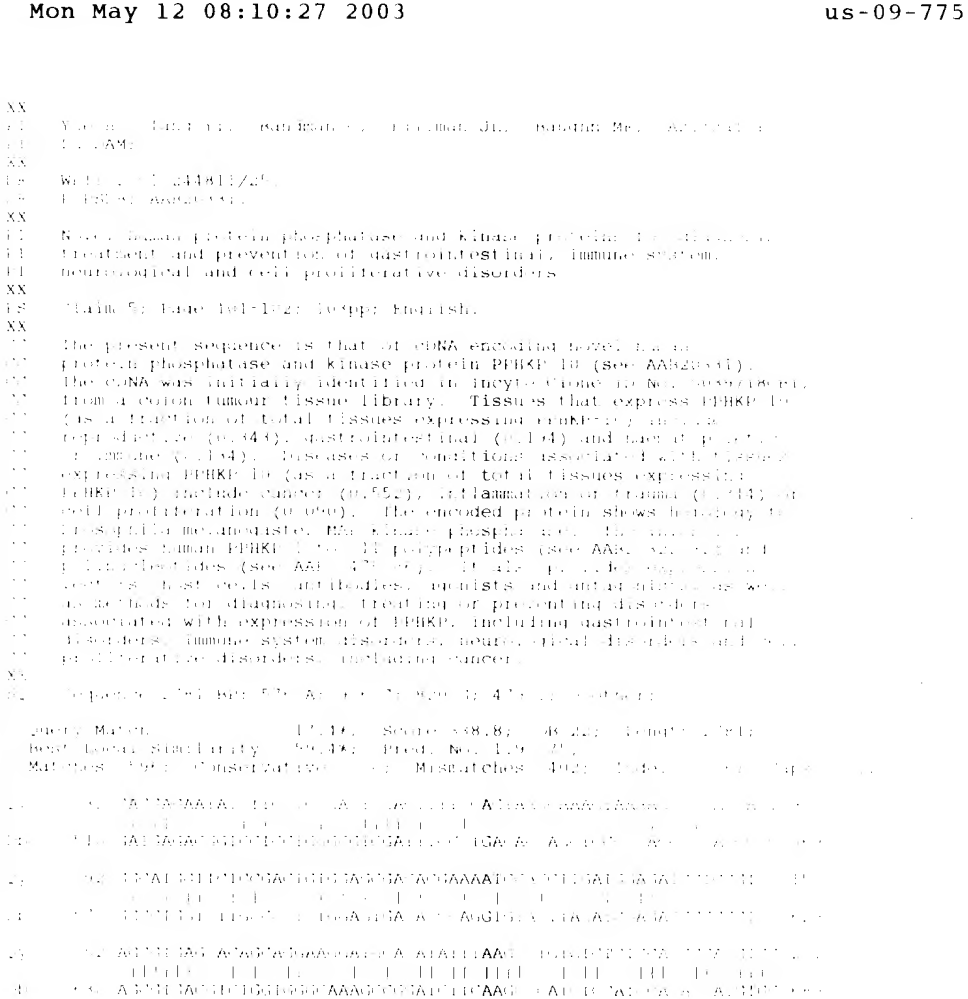
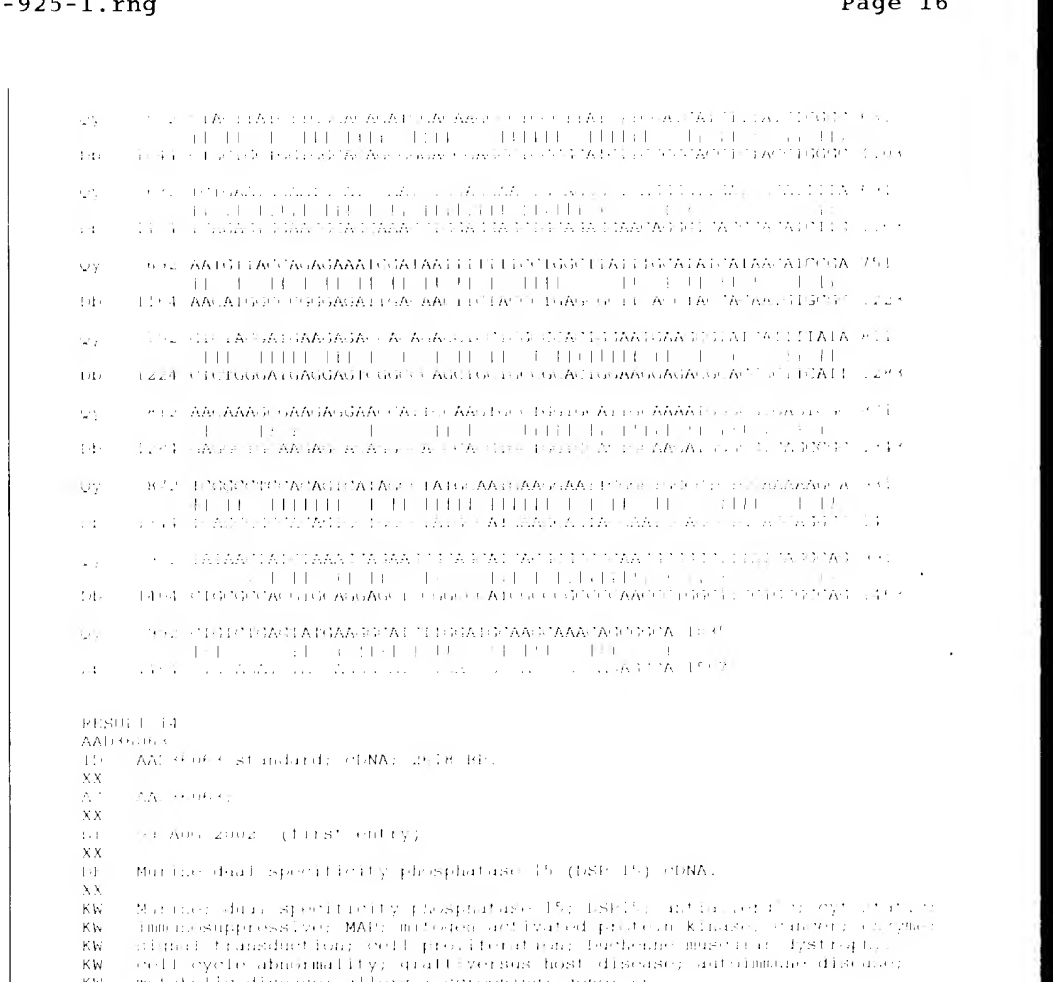
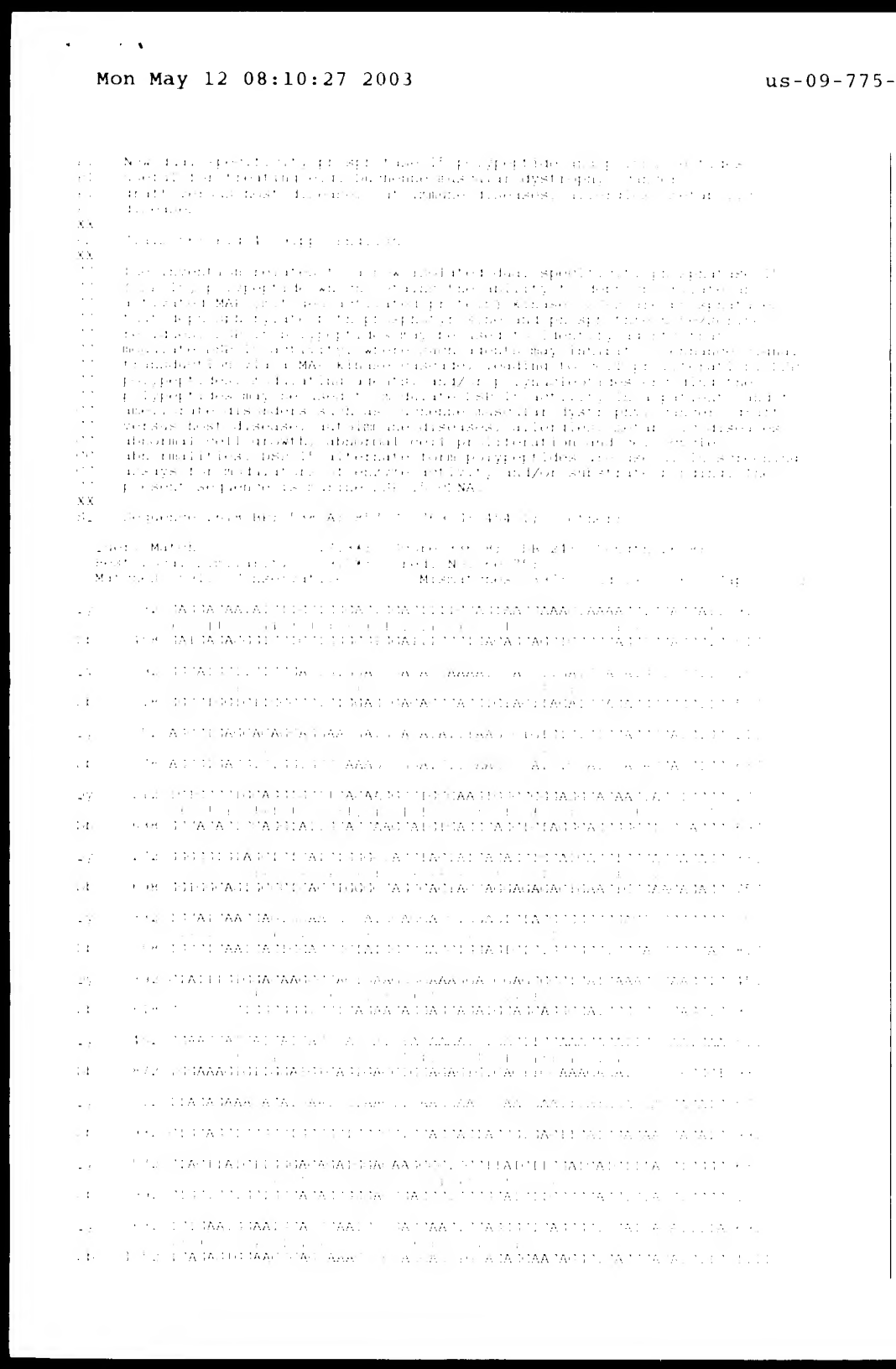


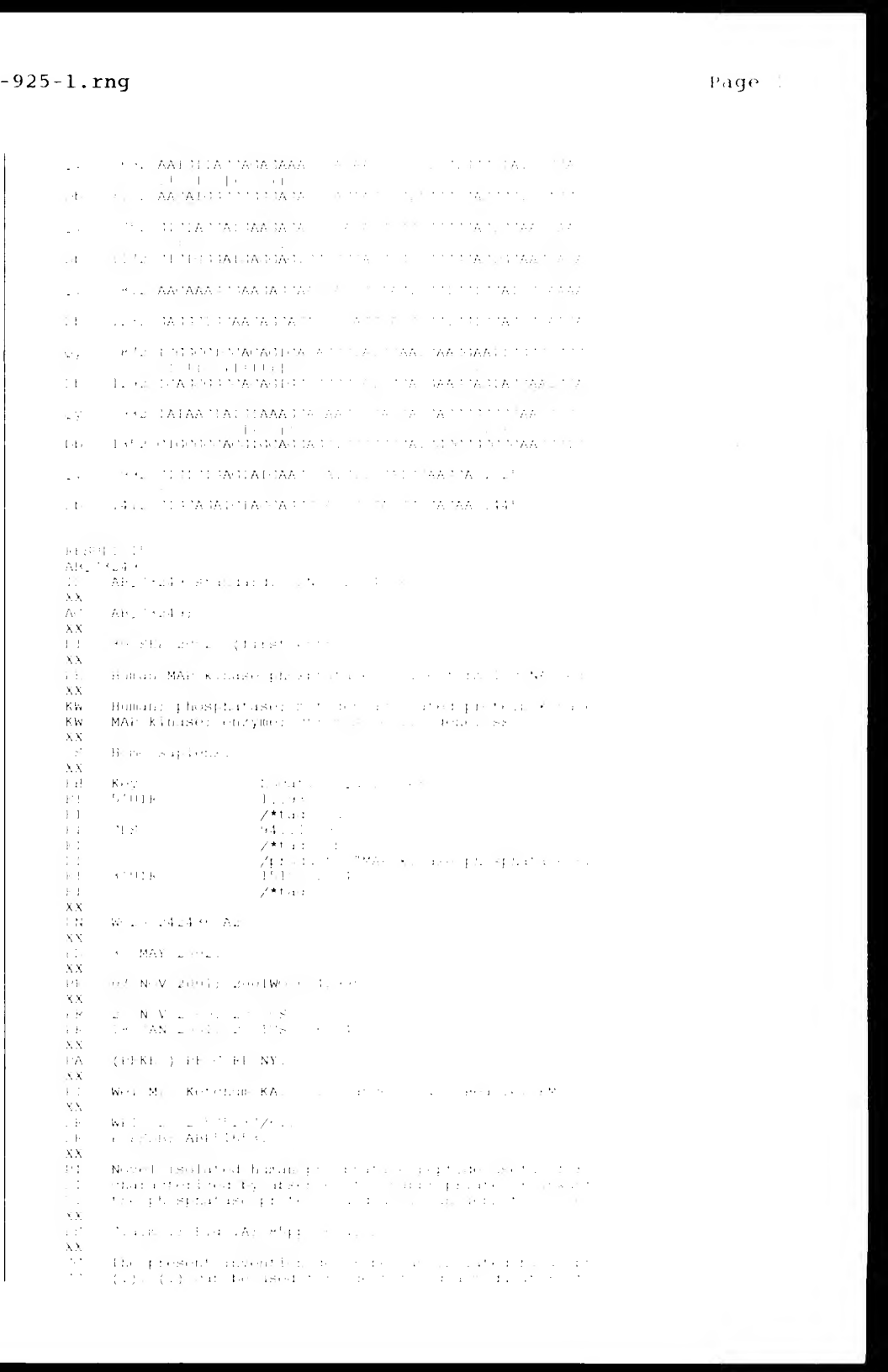


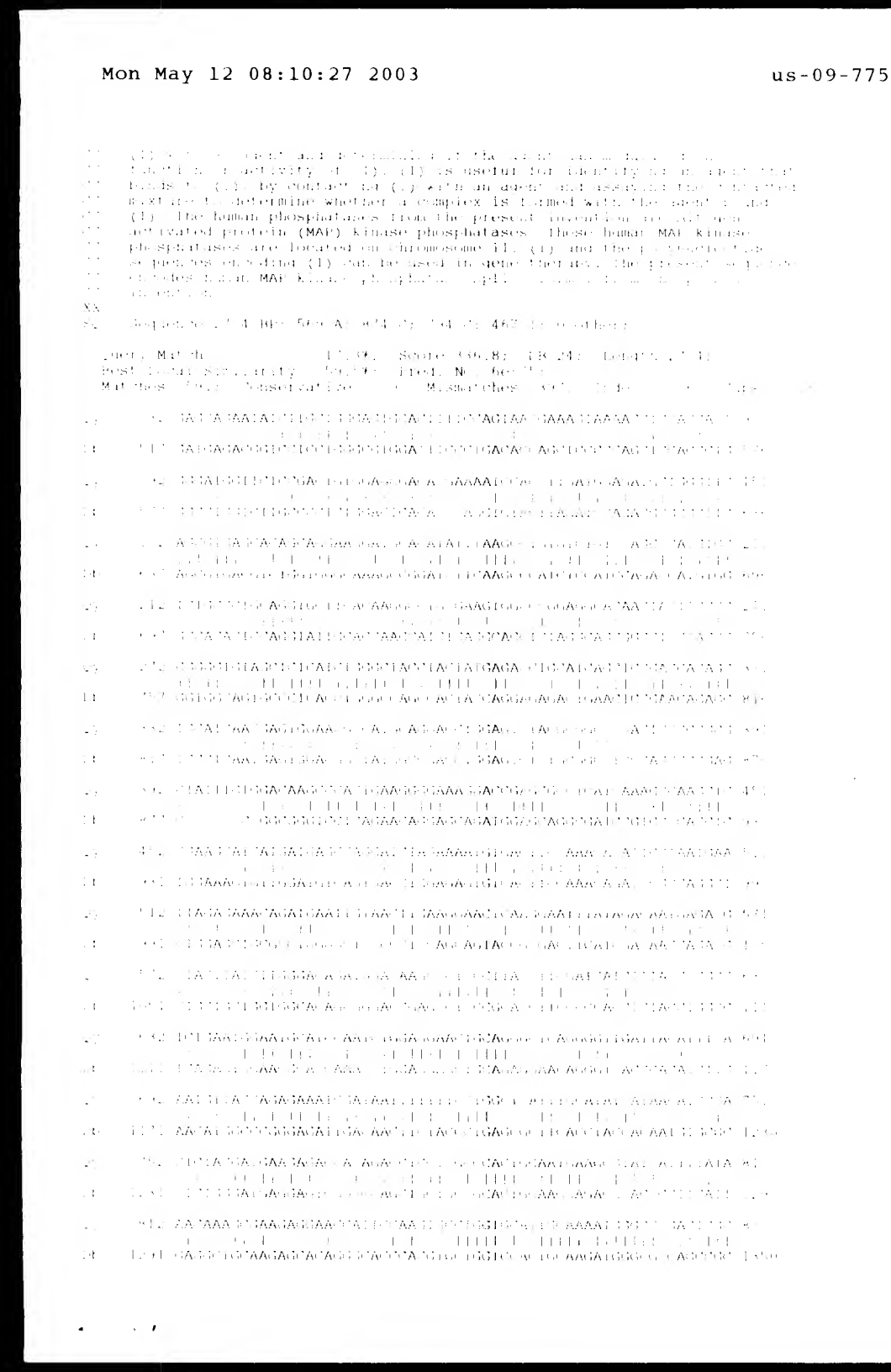


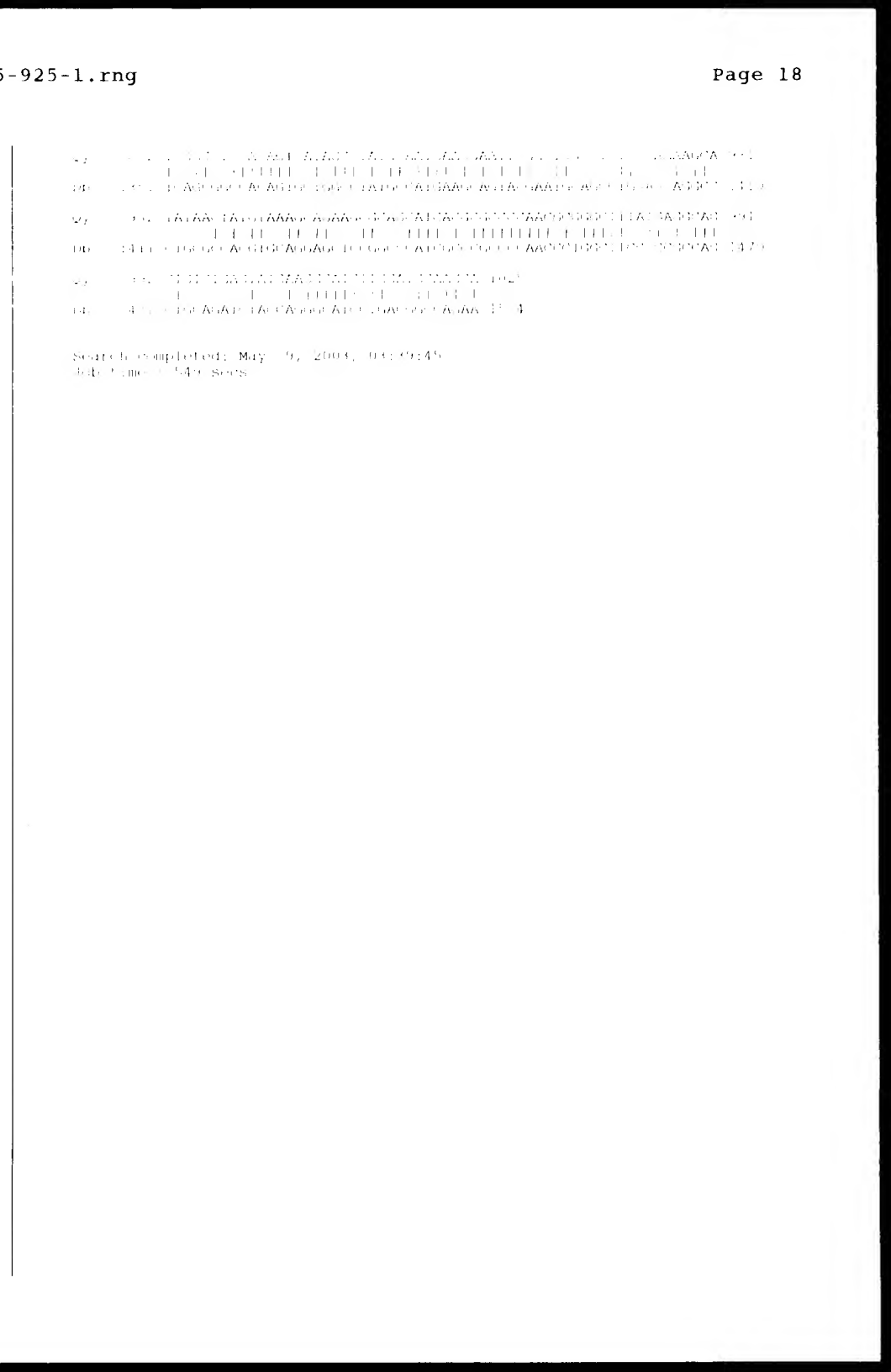


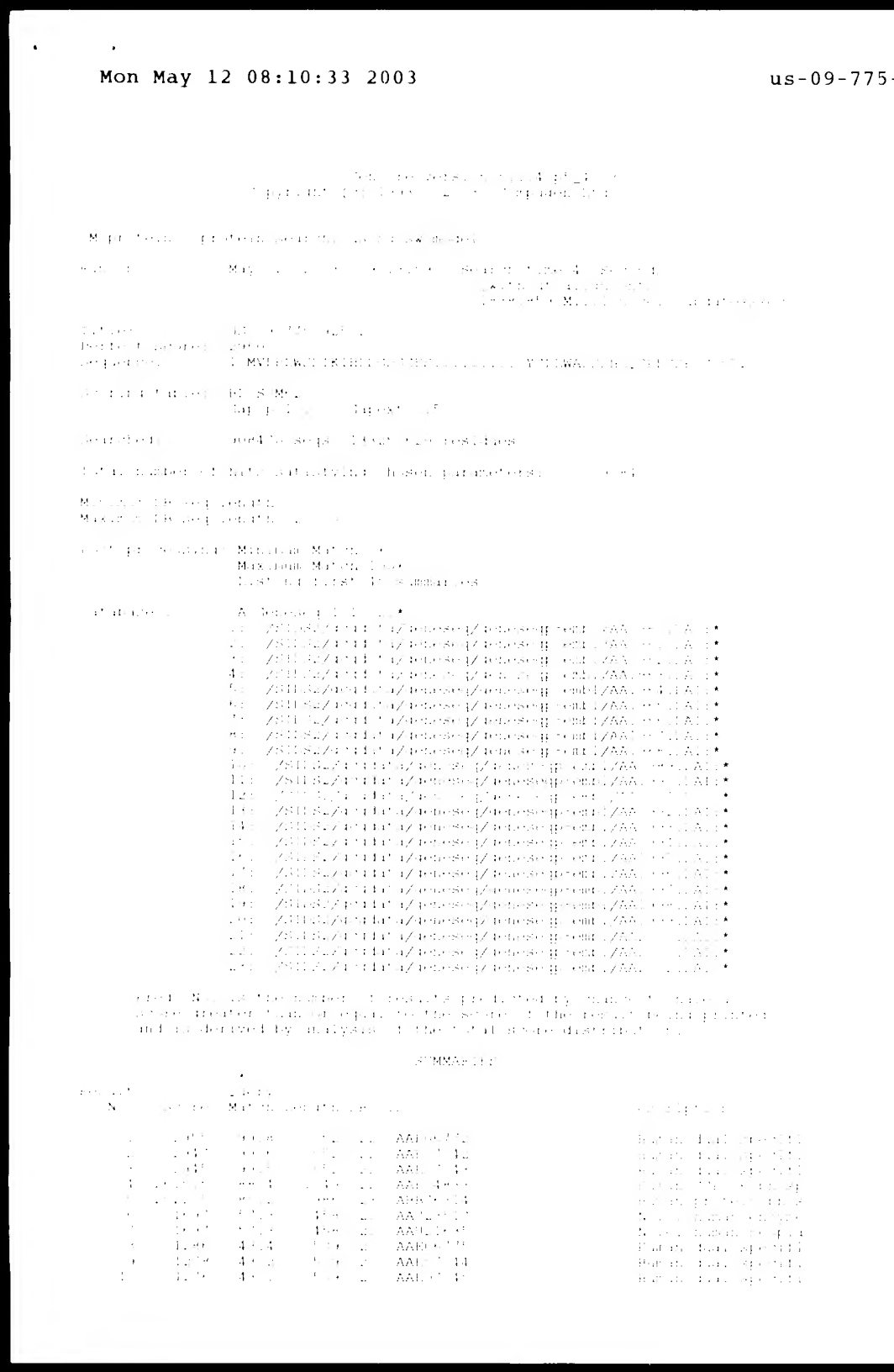


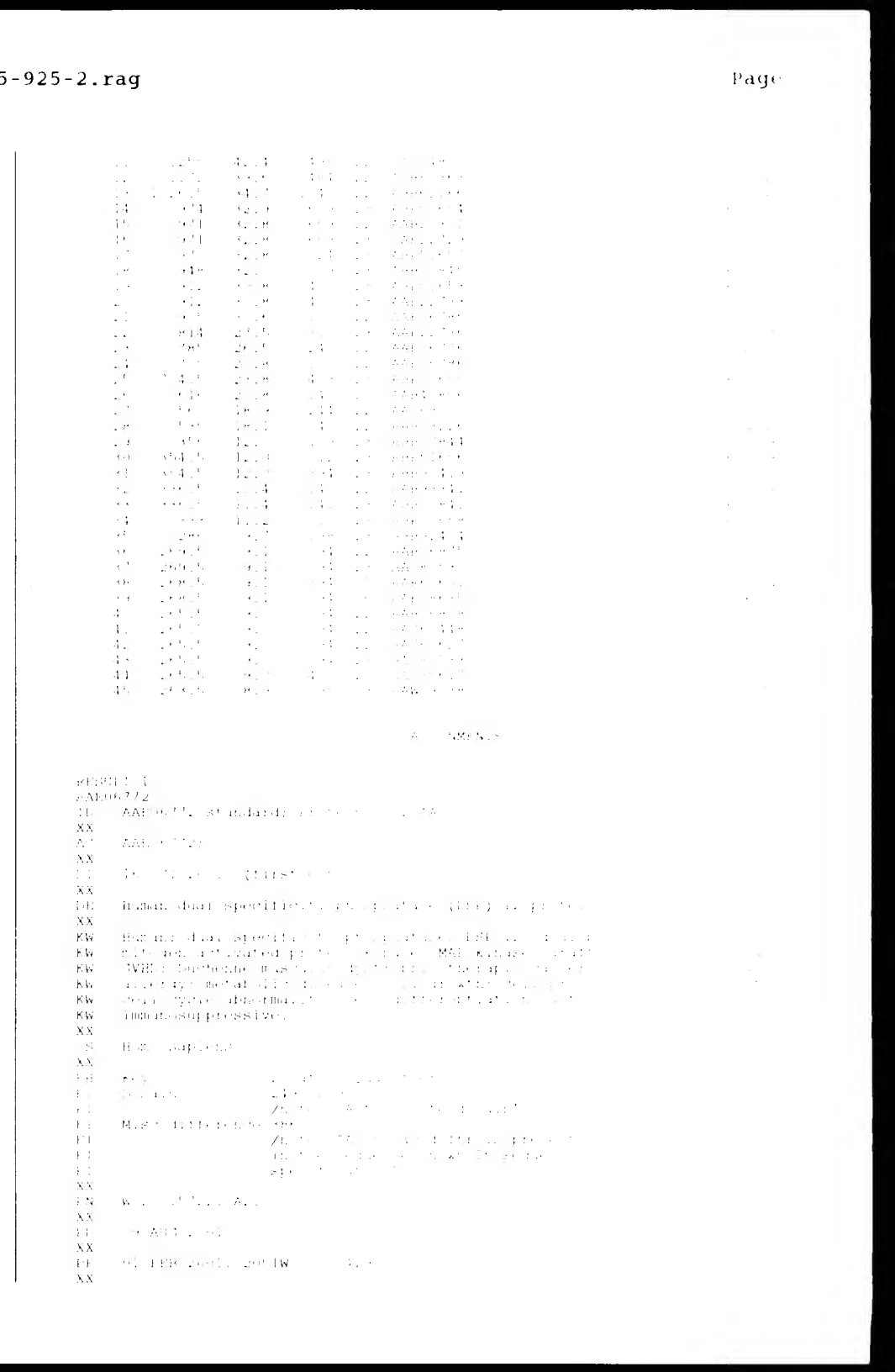






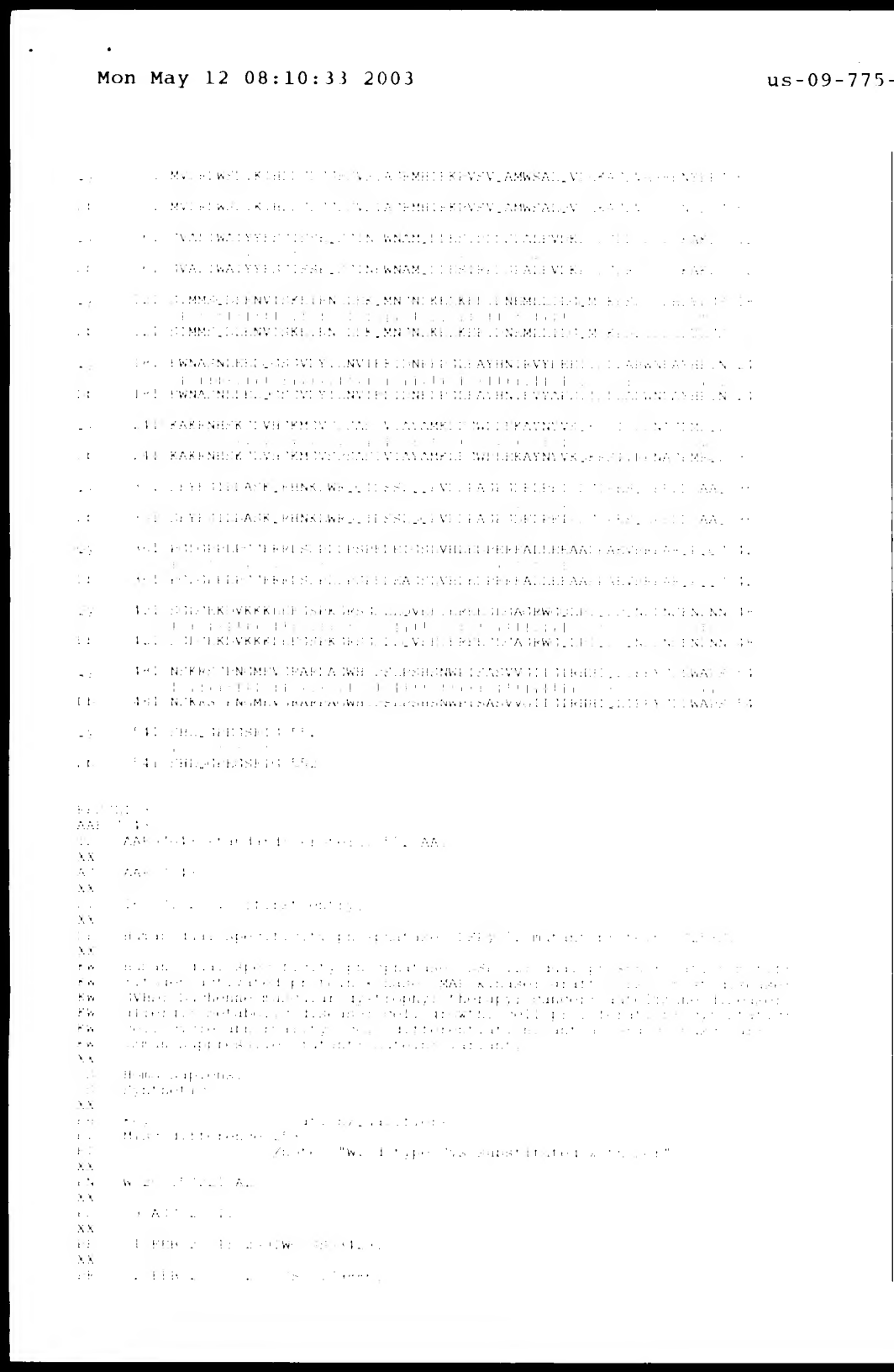


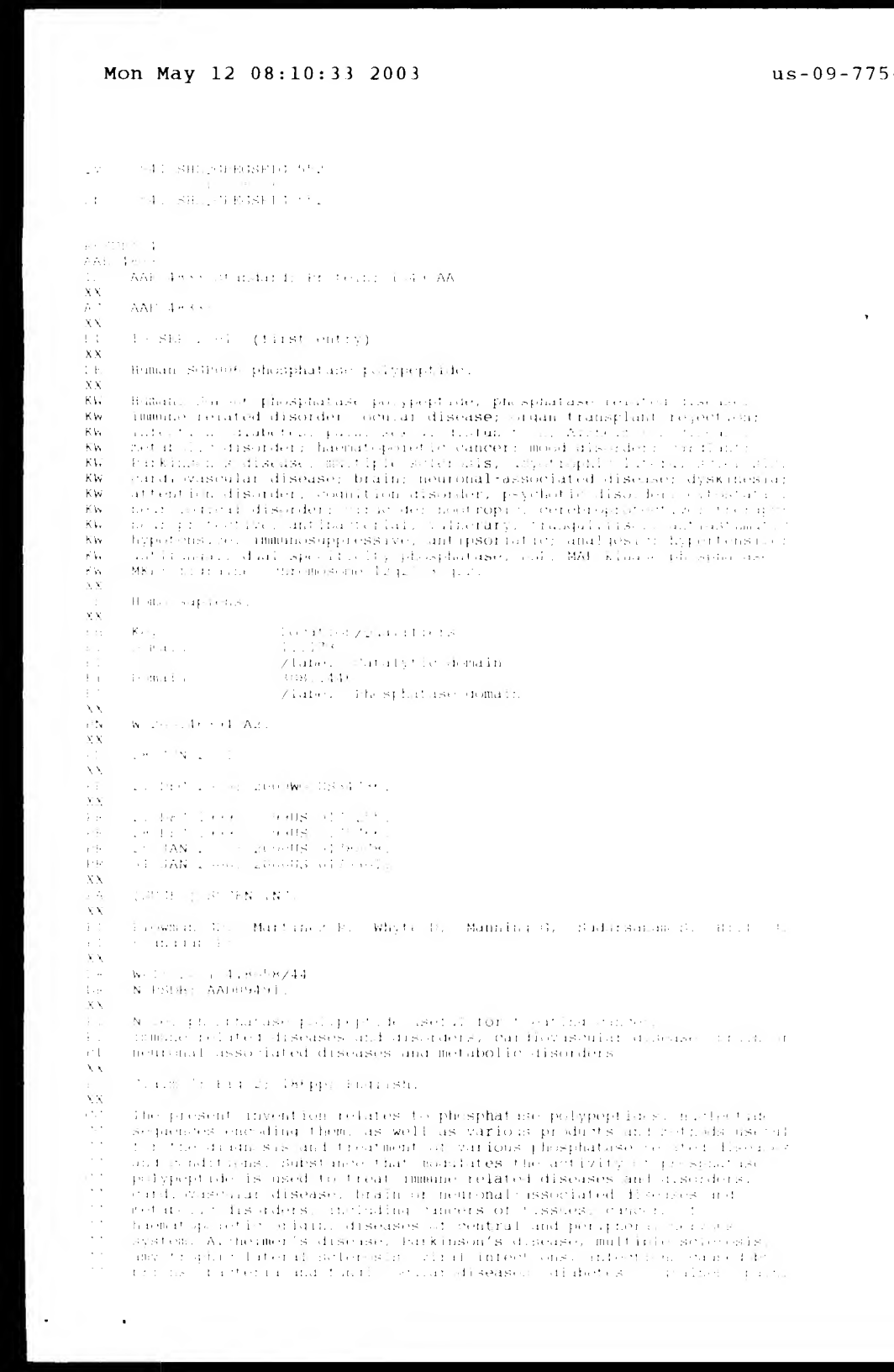




RN [1]
RP 1-552
RA (TEPI) TEPIYK INC.
RT Low-MM Wet Bi
RL WPI; 2001-188882/53.
DR N-PSDB; AAB12961.
XX
PT New isolated dual-specificity phosphatase polypept[illegible] treatin
PT cancer, graft versus host disease, autoimmune diseases, allergies,
PT metabolic diseases, abnormal cell growth and abnormal cell
PT proliferation
XX
PS Disclosure; Page [illegible]; 81pp; English.
XX
CC The present sequence is human dual specificity phosphatase (DSP)-1z
CC mutant protein, D222A. Inactivation of cell proliferation activated protein kinase
CC (MAP kinase) is mediated by dephosphorylation of a dual phosphorylation
CC site by DSP which is referred to as MAP kinase phosphatase. An agent
CC that modulates DSP is useful for treating a disorder selected from
CC Duchenne muscular dystrophy, cancer, graft versus host disease (GVHD),
CC autoimmune diseases, allergies, metabolic diseases, abnormal cell growth,
CC abnormal cell proliferation and cell cycle abnormalities. DSP is useful
CC for identifying antibodies and other agents that inhibit DSP 1z and/or
CC DSP is activity. DSP and the agents identified are useful for
CC modulating cell proliferation, differentiation and survival. DSP is
CC useful in screening assays for modulators of enzyme activity and
CC substrate binding and for dephosphorylating a substrate of DSP 1z or
CC DSP 13.
CC Note: The present sequence is not shown in the specification, but
CC derived from the DSP 1z sequence (AAB12961) given as SEQ ID NO 2 in
CC figure 2.
XX
SQ Sequence 552 AA;

Query Match 99.6%; Score 2047; DB 22; Length 552;
Best Local Similarity 99.6%; Pred. No. 1.2e-259;
Matches 550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;





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PR 25-OCT-2000; 2000US-0241805.
PR 25-OCT-2000; 2000US-0241806.
PR 01-NOV-2000; 2000US-0244137.
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PR 08-NOV-2000; 2000US-0246476.
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PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246537.
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PR 08-DEC-2000; 2000US-0251909.
PR 08-DEC-2000; 2000US-0251910.
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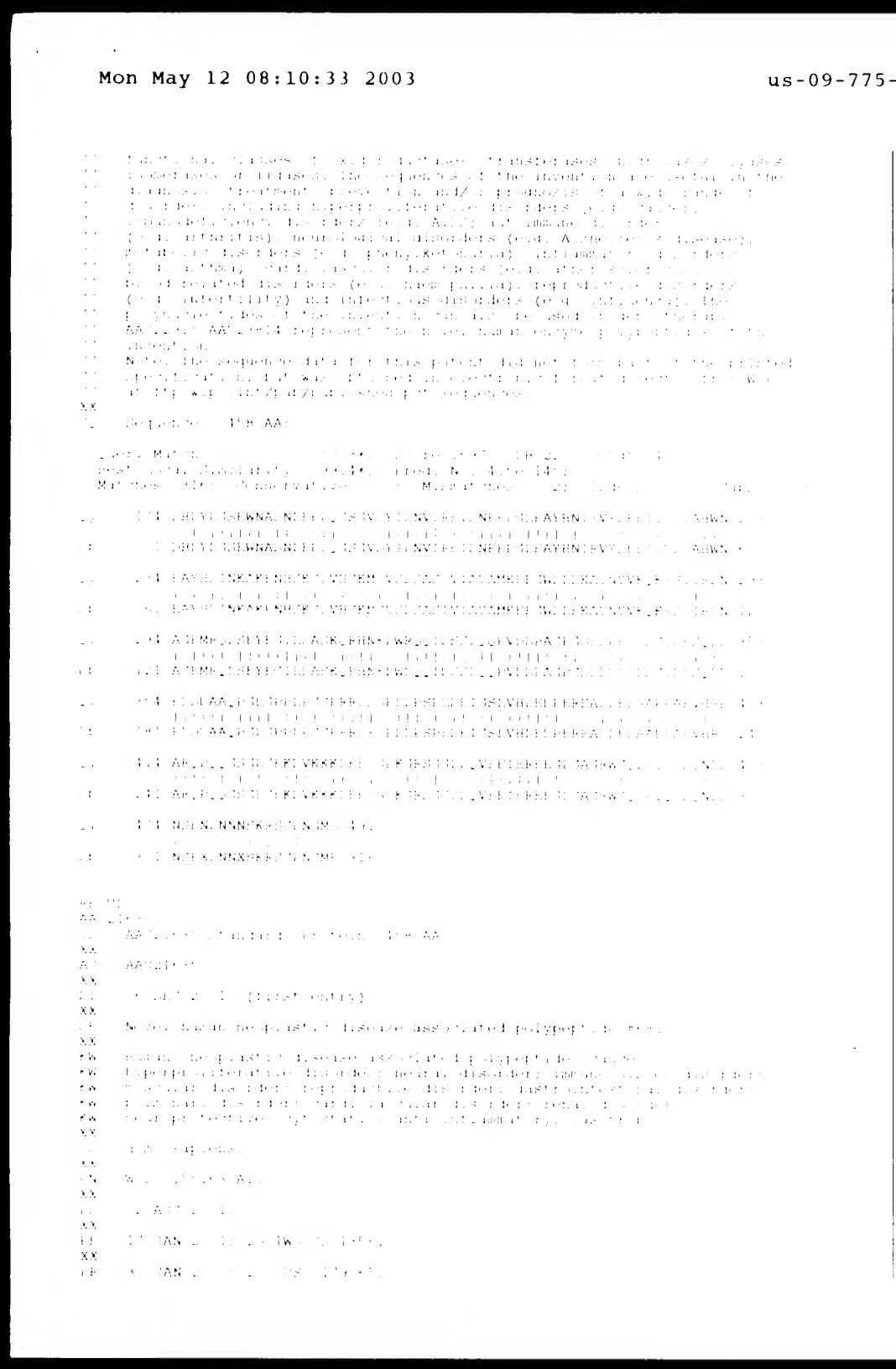
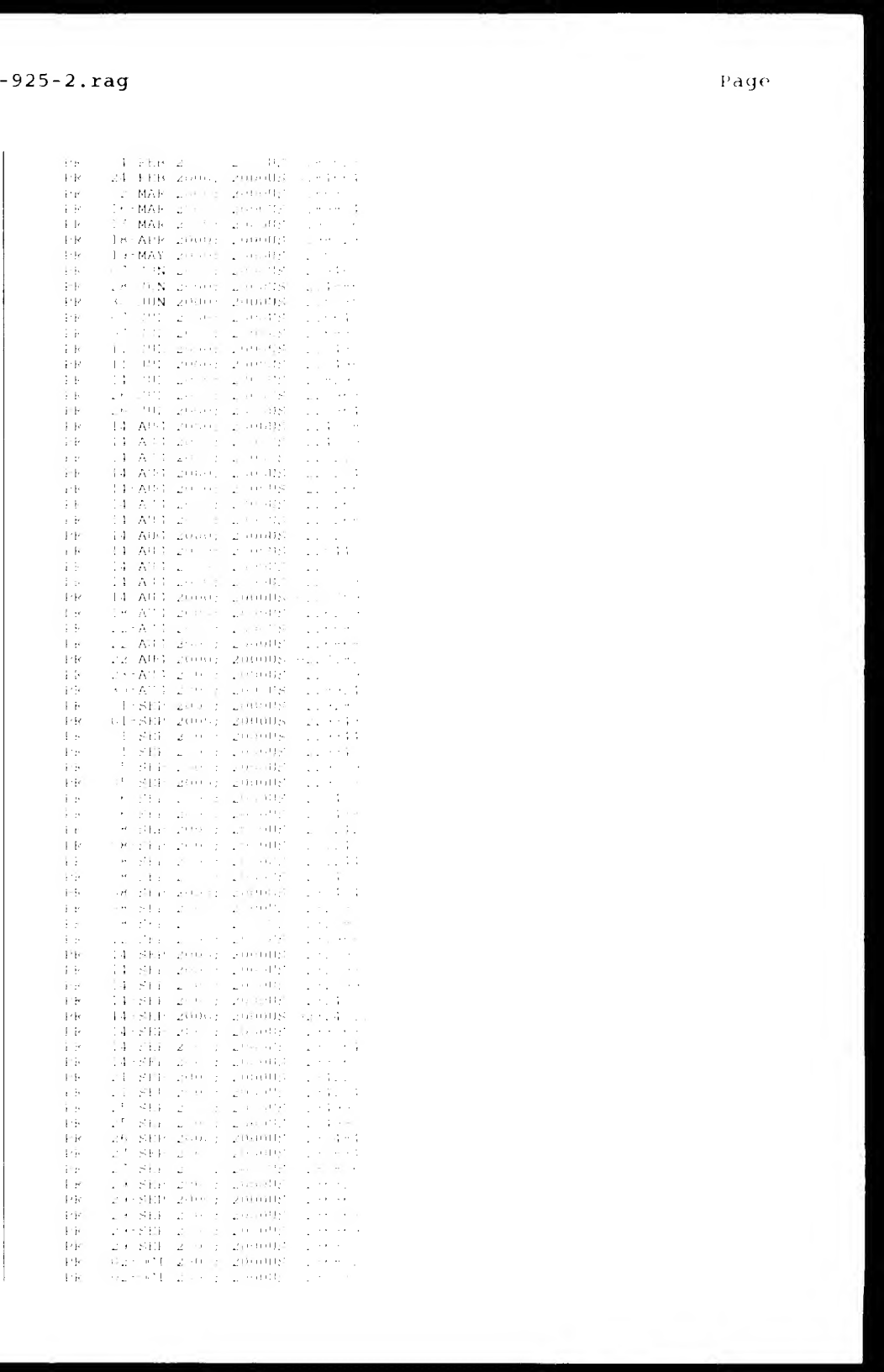
PR 05-JAN-2001; 2001US-0259678.
XX
PA (GEMA) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
DR N-PSDB; AAS41987.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing
PT pre-cardiac, bicuspid neural, immune system, muscular, hepatic cancer,
PT pulmonary cardiovascular, renal, prostate disorders and AIDS
PT infection
XX
PS Claim 11; SEQ ID NO 1513; 218pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41084) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention are useful for





[illegible]

XX

PT Claim 11; SEQ ID No 362; 687pp; English.

XX

CC The present invention relates to the isolation of novel human neoplastic
CC disease associated polypeptides, and cDNA (AAS54767 AAS54768) and DNA
CC sequences encoding for these polypeptides. The sequences of the
CC invention are useful in the diagnosis, treatment, prognosis and/or
CC prognosis of disorders involving neoplastic disease such as
CC hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder
CC cancer, brain stem glioma, adrenal liver cancer, childhood cerebellar
CC astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may
CC also be useful for treating other disorders such as bone disorders,
CC immune system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
CC and renal disorders. The polynucleotide sequences of the invention are
CC also useful in gene therapy. AAU21568 AAU21851 represent the novel human
CC neoplastic disease associated polypeptides of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 408 AA;

Query Match 57.6%; Score 1597; DB 22; Length 408;
Best Local Similarity 99.4%; Pred. No. 4.5e-141;
Matches 316; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MRVTGLRENVANSNLFLSLQNVDVTLNVTSECTDNEFTCSFVATHRDCYVTFDTVSFLNSMDN 60

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Db 61 TAADLQKAKEENLSLEQVATFMVVLSSKEKLAVAAMEDFVKEIERAVNTVTPKFIFFENKTV 120

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Db 121 AGLMKQLESATEGTLDASSQHTNKLWRQAFLQSIQQGFVLDLAGFSDFLFEFSLKDFESQIP 180

Qy 181 FLDDAAQDFGLGPPLPCCERRLSDPLLPSPEDEIGSLVHELEDPEREALGEAAGPALVHRPL 240

Db 181 FLDDAAQDFGLGPPLPCCERRLSDPLLPSPEDEIGSLVHELEDPEREALGEAAGPALVHRPL 240

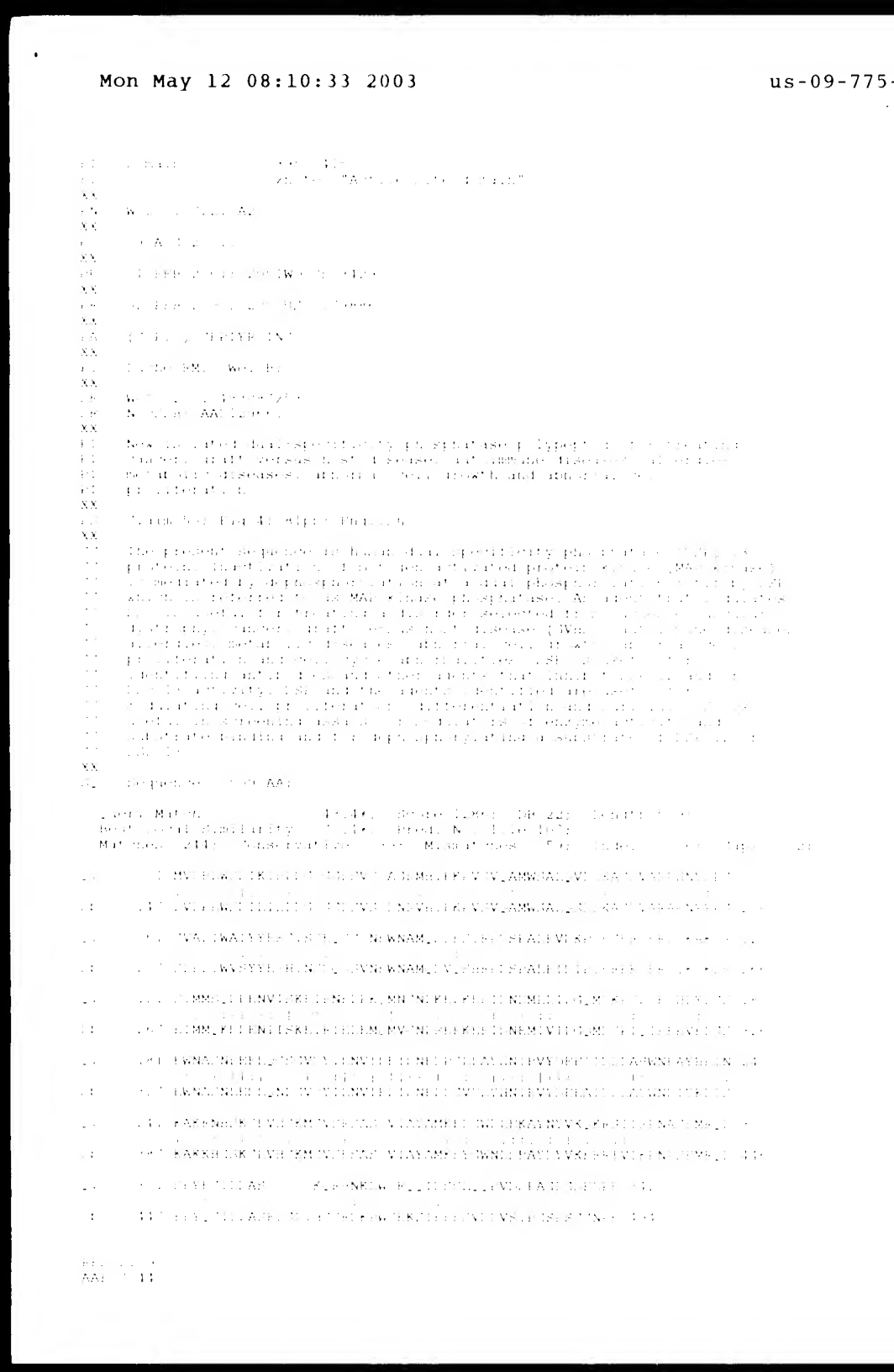
Qy 241 APQDQQVALCEKDVKKKLLRSPKGPSSSLLVEIEEEEEEEGSAGPWGLGPLNSL 297

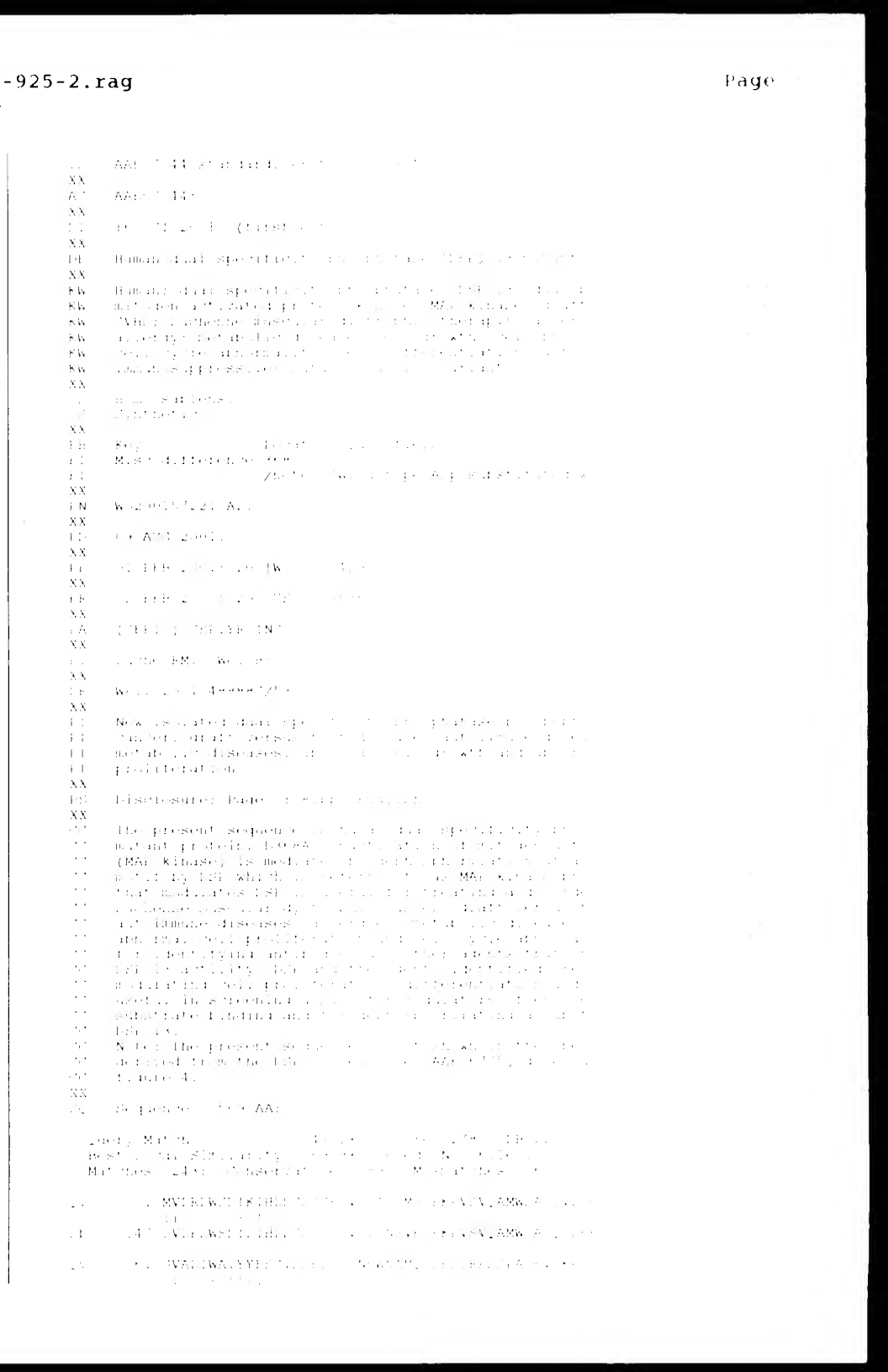
Db 241 APQDQQVALCEKDVKKKLLRSPKGPSSSLLVEIEEEEEEEGSAGPWGLGPLNSL 297

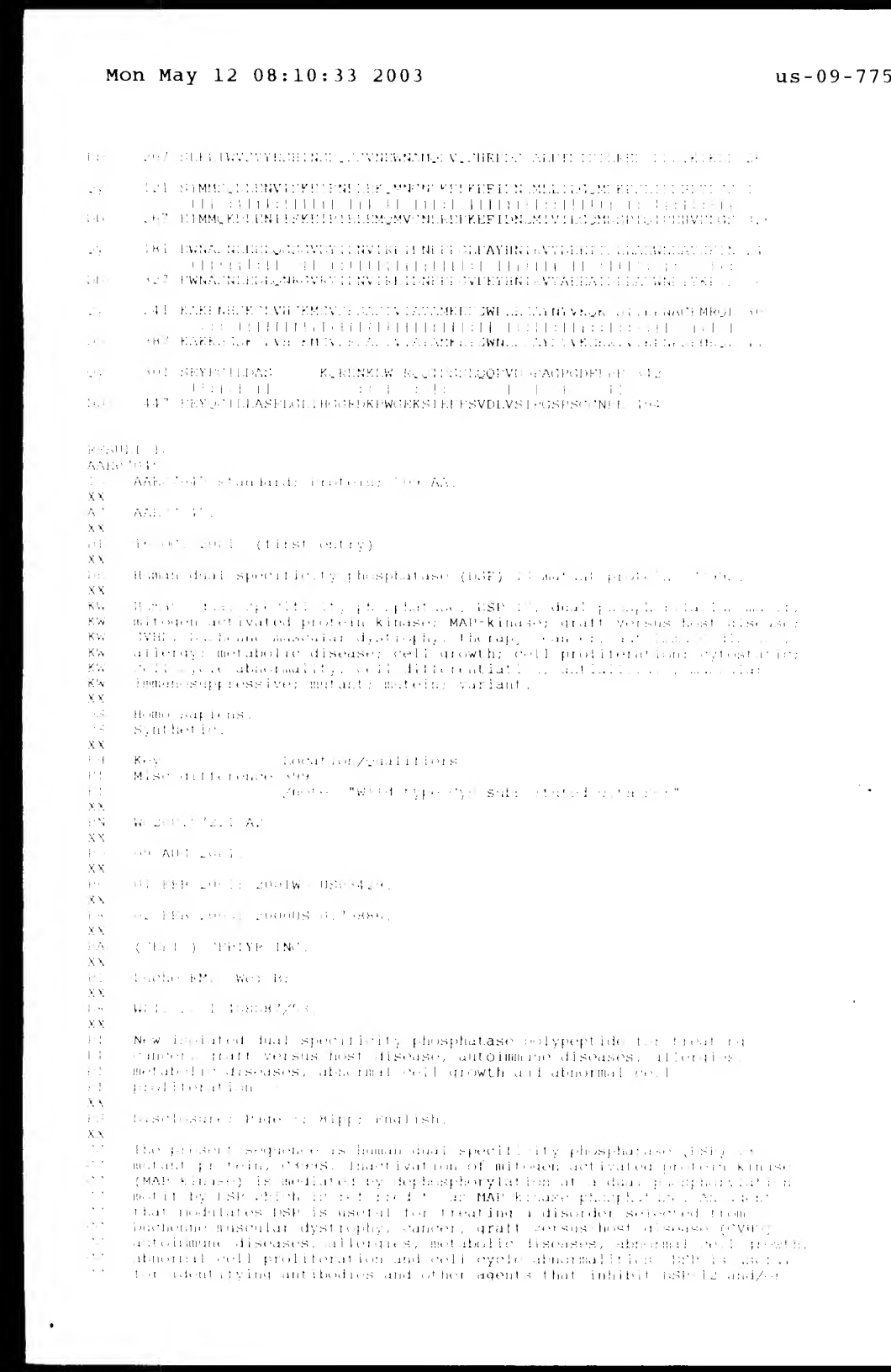
Qy 298 NSENLNNNSKRSCPNGME 315

Db 298 NSEALNNASKRSCPNGME 315

RESULT 8
AAE00775
ID AAE00775 standard; Protein; 315 AA.
XX
AC AAE00775;
XX
DT 26-OCT-2001 (first entry)
XX
DE Human dual specificity phosphatase (DSP) 15 protein.
XX
KW Human; dual specificity phosphatase; DSP 15; dual phosphorylation motif;
KW mitogen activated protein kinase; MAP kinase; graft versus host disease;
KW VHR; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease;
KW allergy; metabolic disease; wasting; cell proliferation; cell cycle;
KW cell cycle abnormality; cell differentiation; antiarthritic; muscular;
KW immunosuppressive.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

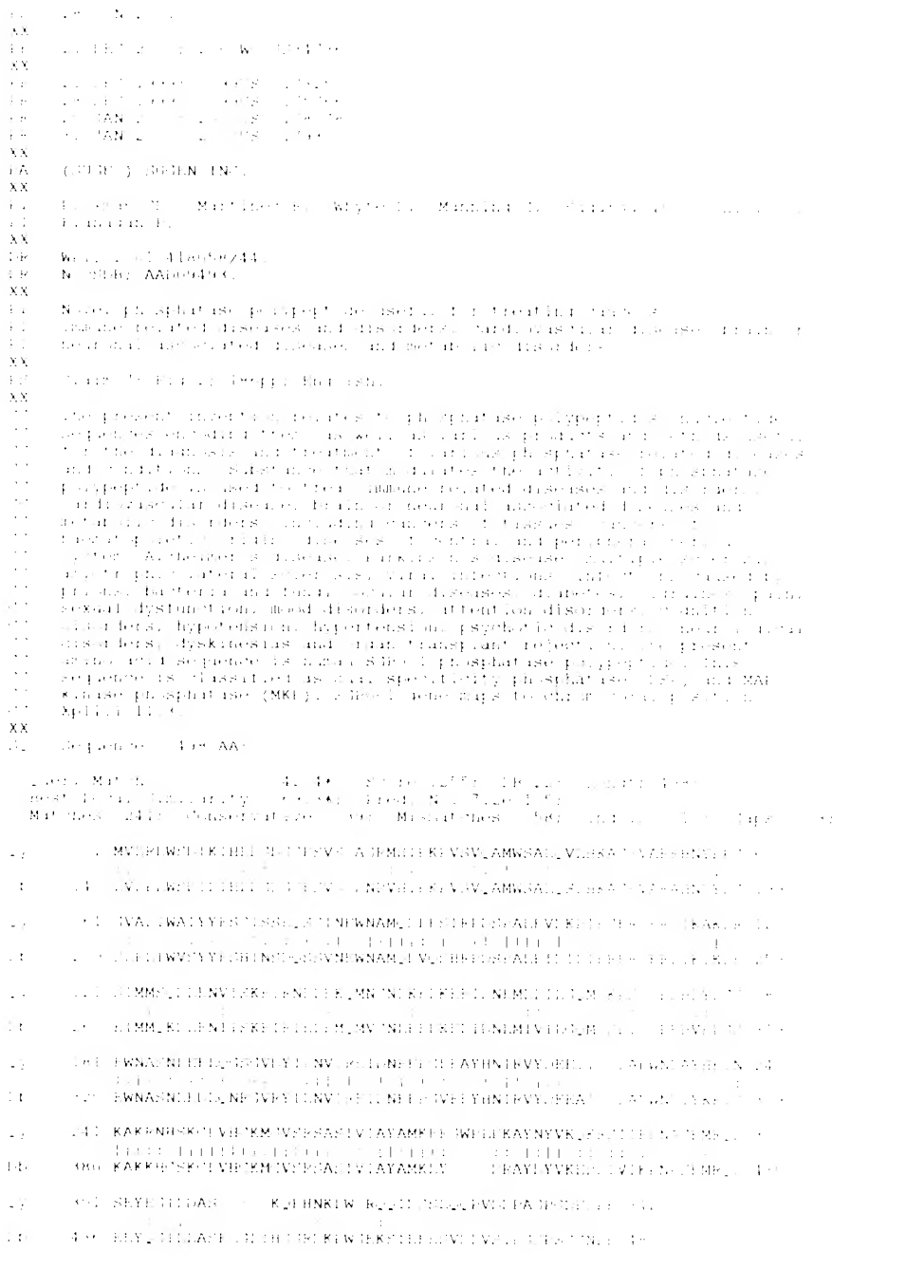


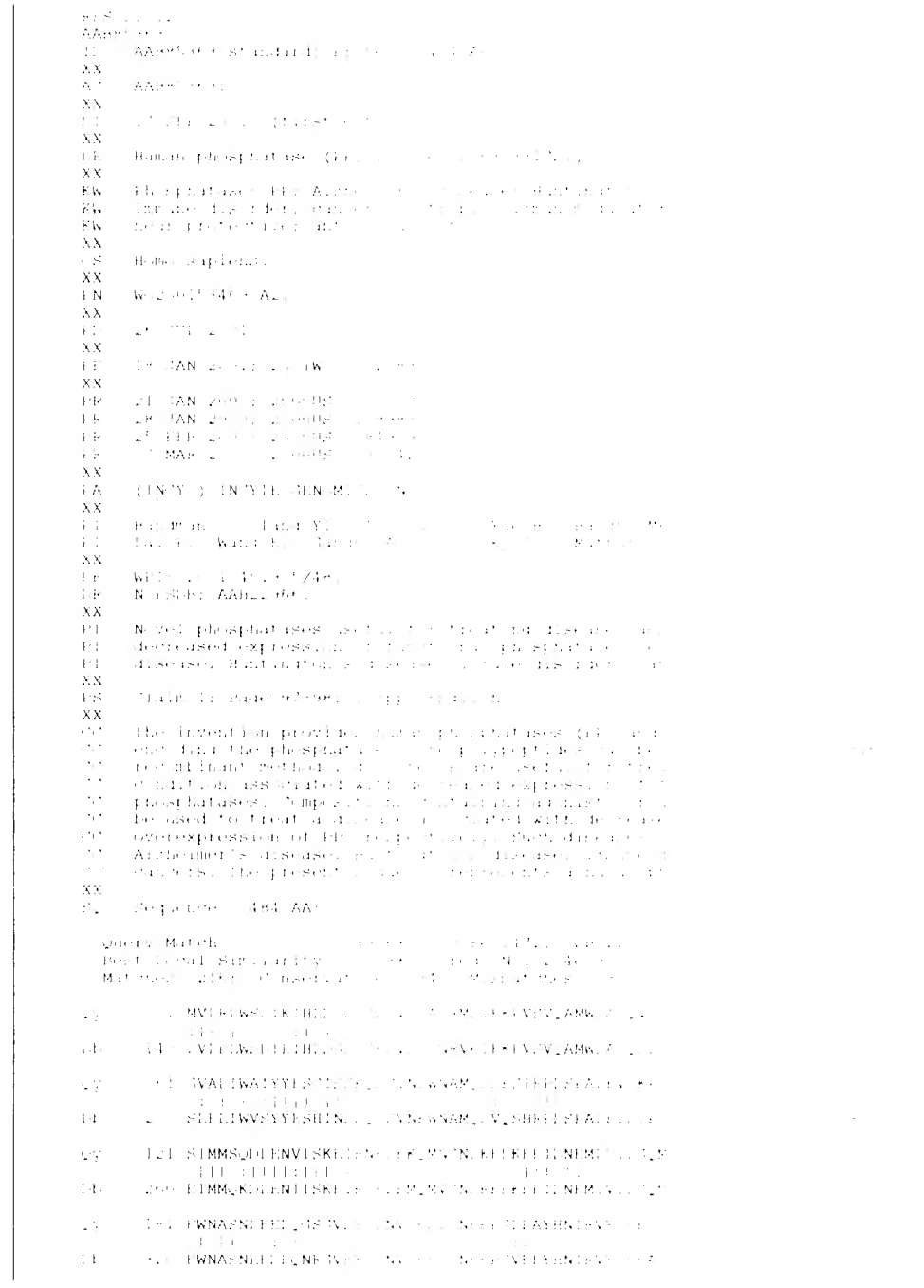


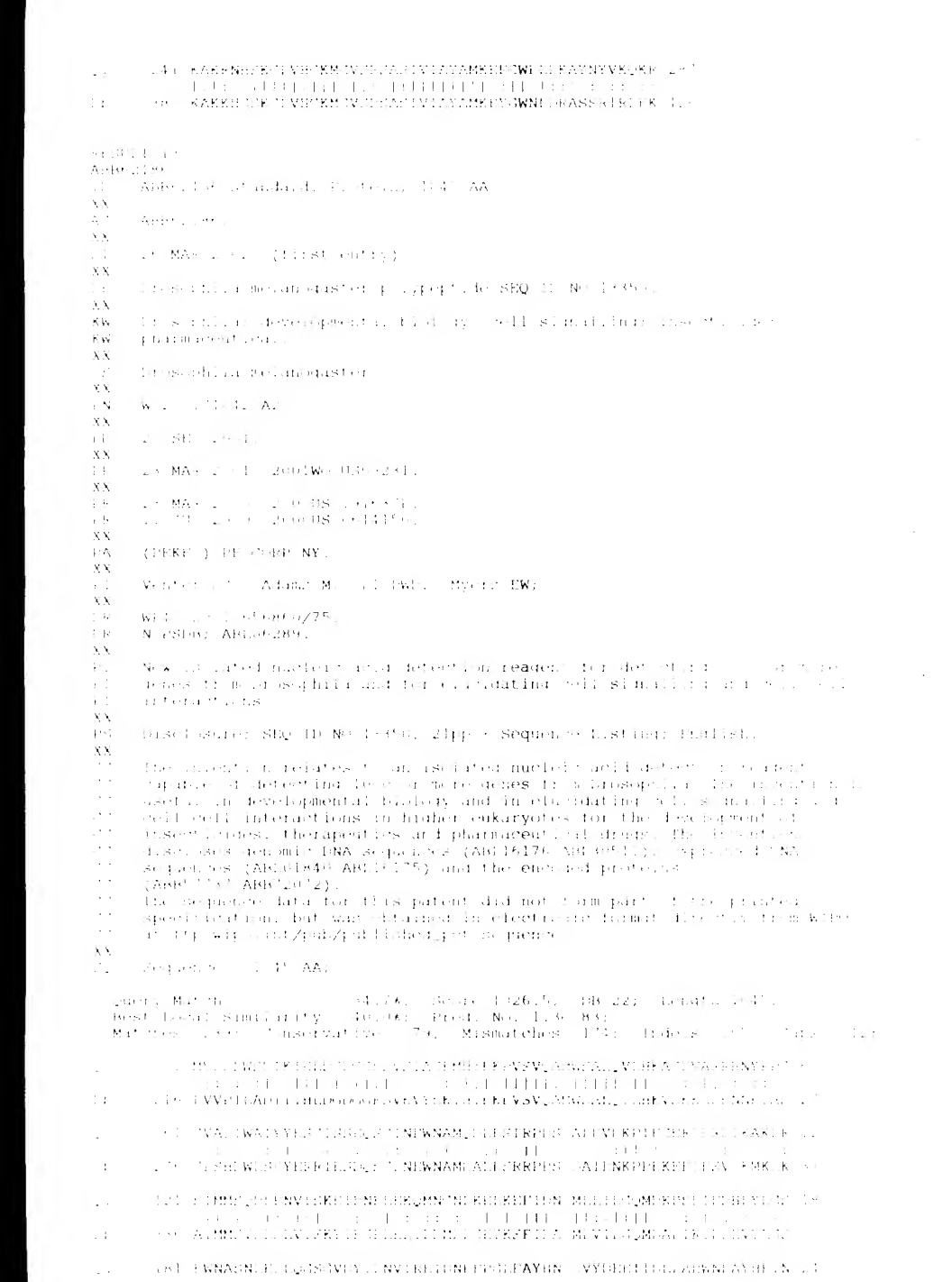


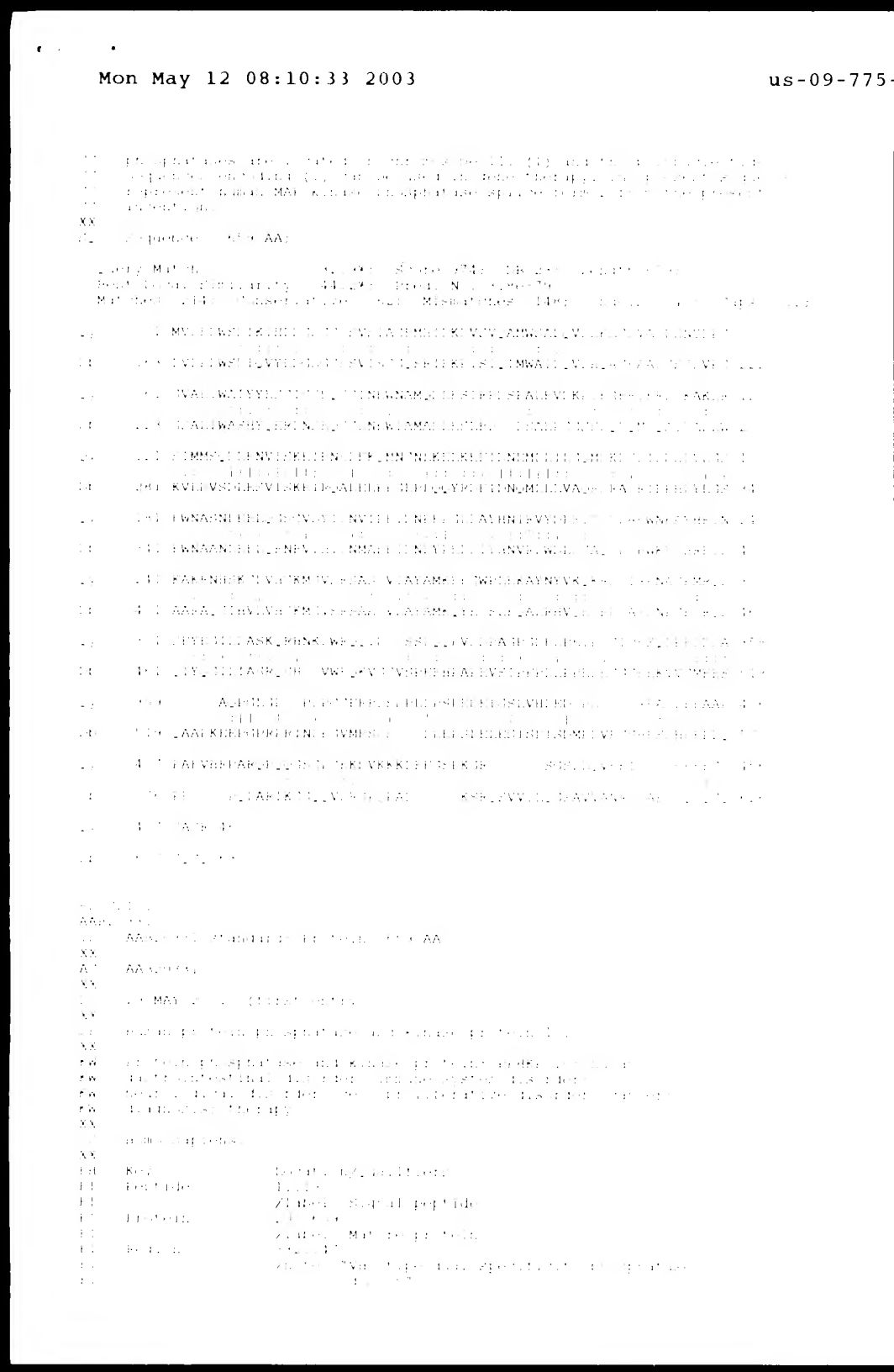
RESULT 1
AAB03845
ID AAB03845 standard; Protein; 509 AA.
XX
AC AAB03845;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human dual specificity phosphatase (hDP) 2 amino acid protein.
XX
KW Dual specificity phosphatase; hDP; dual phosphorylation; mitogen activated protein kinase; MAP-kinase; graft versus host disease; GVHD; Crohn's disease; autoimmune dystrophy; therapy; cancer; arthritis; allergy; metabolic disease; cell growth; cell proliferation; cytostatic; cell cycle abnormality; cell differentiation; antibody; vaccine; immunosuppressive; mutant; protein; variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 499
FT /note= "Wild-type cys at pos. replaced by ser"
XX
PN WO200146394-A2.
XX
PD 28-JUN-2001.
XX
PF 20-DEC-2000; 2000WO-US034294.
XX
PR 20-DEC-1999; 99US-0466476P.
XX
PA (TEIJ) TEIJIN LTD.
XX
PI Tsuchiya M; Wei B;
XX
DR WPI; 2001-418967/44.
XX
PT New isolated dual specificity phosphatase polypeptide for treating cancer, graft versus host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth and abnormal cell proliferation
XX
PS Disclosure; Page 1; 81pp; English.
XX
CC The present sequence is human dual specificity phosphatase (hDP) 2 mutant protein, C499S. Inactivation of mitogen activated protein kinase (MAP kinase) is mediated by dephosphorylation at a dual phosphorylation motif by hDP. hDP is a MAP kinase phosphatase. As hDP that modulates hDP is useful for treating a disorder selected from ischemic muscular dystrophy, cancer, graft versus-host disease (GVHD), autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities. hDP is also for identifying antibodies and other agents that inhibit hDP2 activity. hDP and the agents identified are useful for modulating cell proliferation, differentiation and survival. hDP is useful in screening assays for modulators of enzyme activity and substrate binding and for dephosphorylating a substrate of hDP-2 or hDP-1.
CC Note: The present sequence is not shown in the specification, but is derived from the hDP-2 sequence (AAB03775) given as SEQ ID NO:6 in figure 4.
XX
SQ Sequence 509 AA;

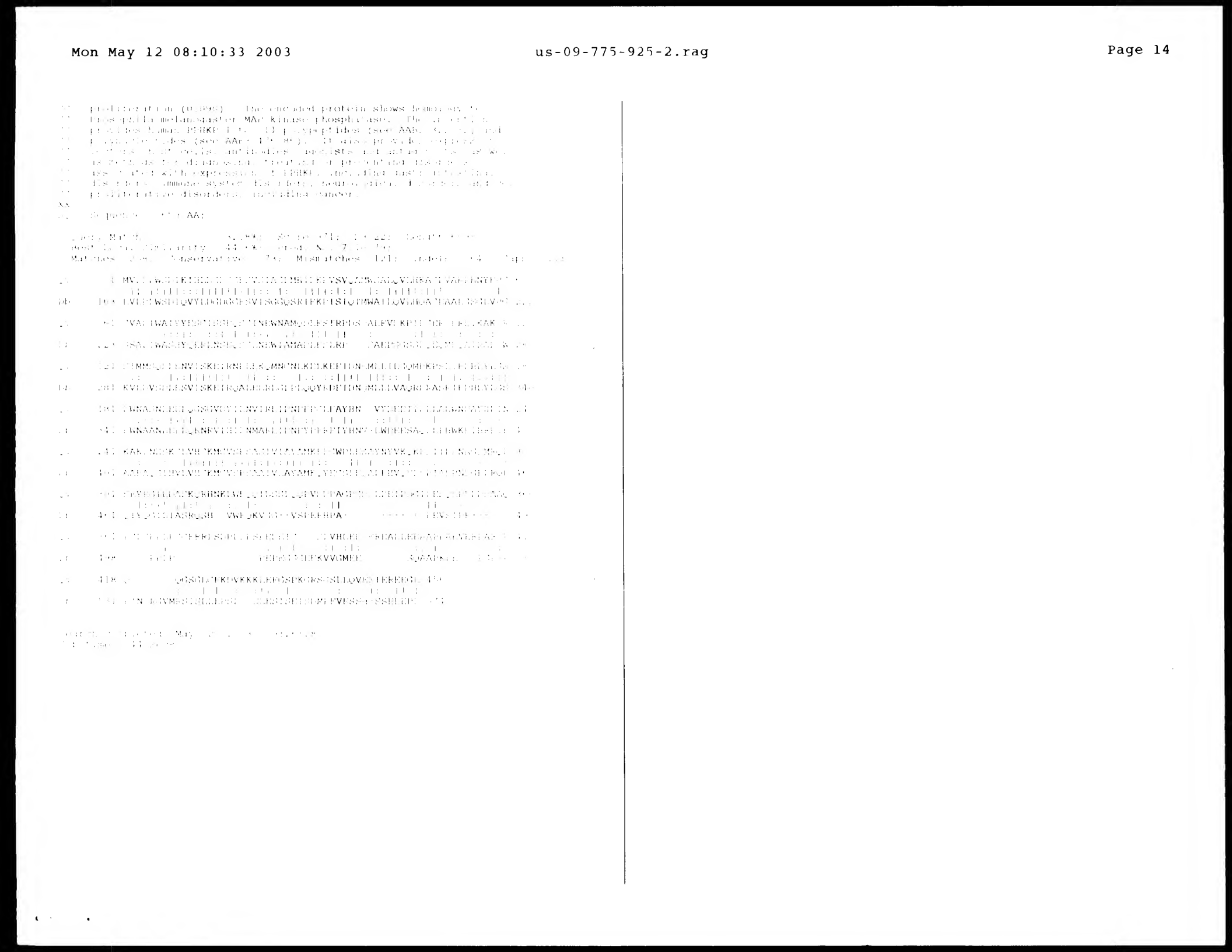
RESULT 11
AAB03845
ID AAB03845 standard; Protein; 498 AA.
XX
AC AAB03845;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human SSH001 phosphatase polypeptide.
XX
KW Human; SSH001 phosphatase polypeptide; phosphatase related disease; immune related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction; Alzheimer's disease; metabolic disorder; haematopoietic cancer; mood disorder; cardiac; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain, neuronal associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; analgesic; hypertensive; antineoplastic; dual specificity phosphatase; hDP; MAP kinase phosphatase; MKP; migraine; chromosome Xp11.4-11.3.
XX
OS Homo sapiens
XX
FH Key Location/Qualifiers
FT Domain 1..179
FT /label= Catalytic_domain
FT Domain 307..441
FT /label= Phosphatase_domain
XX
PN WO200146394-A2.
XX

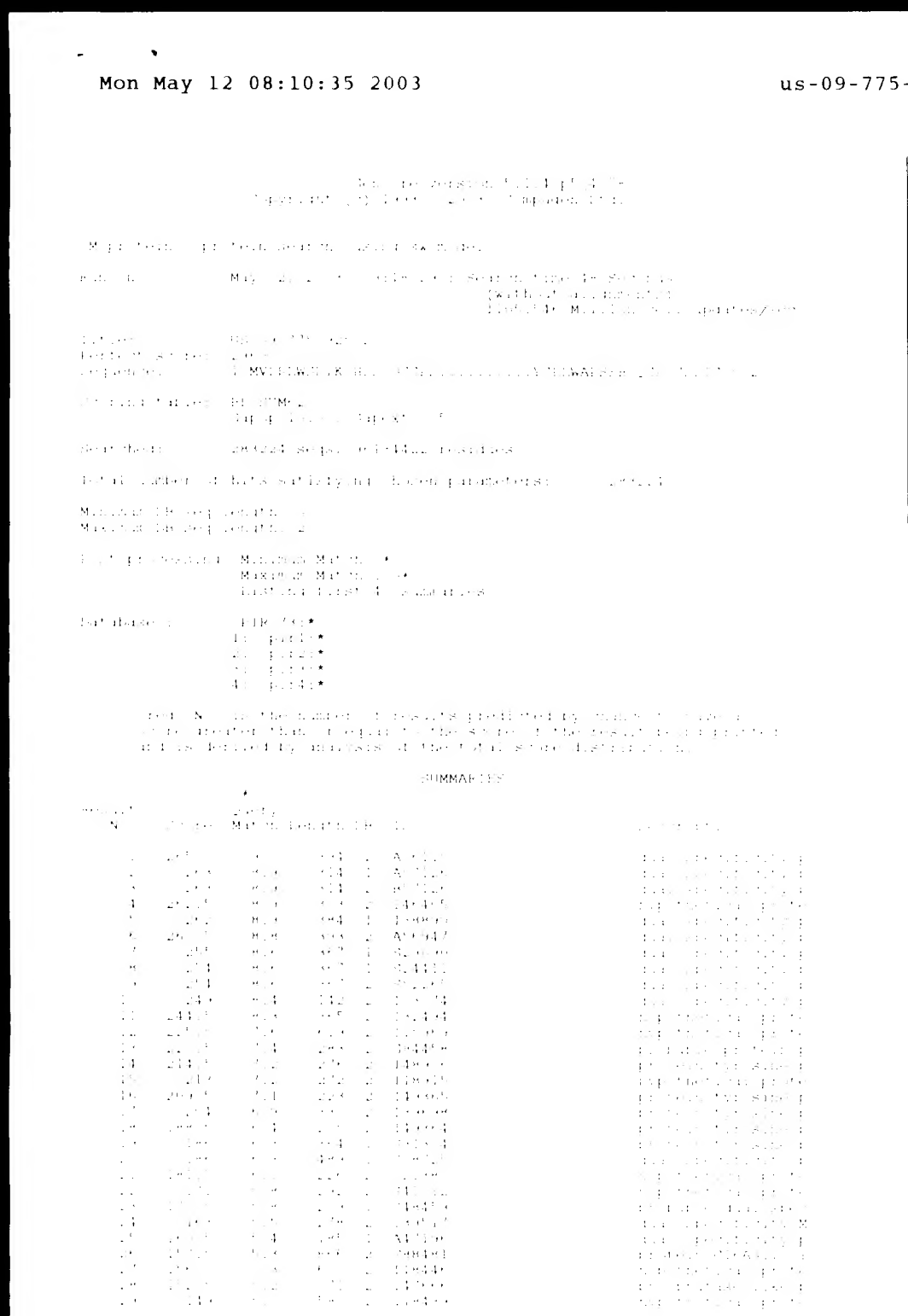












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A57126
dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 2 - mouse
N;Alternate names: mitogen-induced nuclear protein-tyrosine-phosphatase (MP-1
C;Species: Mus musculus (house mouse)
C;Date: 02-Nov-1995 #sequence_revision 02-Nov-1995 #text_change 21-Apr-1999
C;Accession: A57126
R;Rohan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Krutzsch, H.; Siebenlist, U.; Kel
Science 264, 1766-1766, 1994
A;Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase
A;Reference number: A57126; MUID:94206132; PMID:7684221
A;Accession: A57126
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-314 <KOB>
A;Cross-references: GB:L11329; NID:g599540; PIDN:AAA58279.1; PID:g206176
C;Genetics:
A;Gene: GDB:DUSP2
A;Cross-references: GDB:139209
A;Map position: 2q11-2q11
C;Function:
A;Description: catalyzes the hydrolysis of peptidyl phosphoserine, ph
C;Superfamily: dual specificity phosphoprotein phosphatase 1 VHI type dual specificity
C;Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase
F;1-140/Region: nuclear location signal
F;1-180/Domain: VHI type dual specificity phosphoprotein phosphatase (...) VHI
F;57/Active site: Cys (phosphocysteine intermediate) #status predicted
F;127/Binding site: substrate phosphate (Arg) #status predicted

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Qy      169 PSLIFDHLYYGSEWNKGNLEGQGSVATFGNVTKLLNETEGLLAYENTFVTLEETIDL 228
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Db      175 PVLILPFLTTGSATHAAKKDMLDAIAILALGVSSDATENHFHGHYQYKCTIVTEGHKAD 234

Qy      229 ASWNLAYHENRAKDRESHF-AVDTGMVFMAVNEDASLVSYAMRFTWSFFKSKPEKS 283
            : | || :|| |  :  : |||| :|||||  :|| | :    |||:| :|||||
Db      235 SSWPFMEAILTDAVKDFSGNYKVDQATLGKSATLCLATLMMKKKDVFLLKPETFTGLKRS 294

Qy      284 FTKENAGFMRQLSEYE 300
            :  ||  || || : |
Db      295 VISPNFSFMGQLLQLE 310


RESULT 4
A46405
hypothetical protein DKFZp434O1421.1 - human
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 21-Jun-2002
C;Accession: T46405
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Cassenteber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23034
A;Accession: T46405
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-303 <AAA>
A;Cross-references: EMBL:AL132704
A;Experimental source: adult testis; clone DKFZp434O1421
C;Genetics:
A;Note: DKFZp434O1421.1

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            |  |  ||||| :::|:  : |  |:  :|||:  : | | | | | | :  |:
Db      105 PVLILPFLTTGSATHAAKKDMLDAIAILALGVSSDATENHFHGHYQYKCTIVTEGHKAD 164

Qy      229 ASWNLAYHENRAKDRESHF-AVDTGMVFMAVNEDASLVSYAMRFTWSFFKSKPEKS 283
            : | || :|| |  :  : |||| :|||||  :|| | :    |||:| :|||||
Db      165 SSWPFMEAILTDAVKDFSGNYKVDQATLGKSATLCLATLMMKKKDVFLLKPETFTGLKRS 224

Qy      284 FTKENAGFMRQLSEYE 300
            :  ||  || || : |
Db      225 VISPNFSFMGQLLQLE 240


RESULT 5
I38890
N;Alternate names: dual specificity phosphatase B23; dual specificity phosphatase hVH
C;Species: Homo sapiens (man)
C;Date: 29-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jun-1999
C;Accession: I38890; A55413
R;Kwak, S.P.; Dixon, J.E.
J. Biol. Chem. 270, 1156-1160, 1995
A;Title: Multiple dual specificity protein tyrosine phosphatases are expressed and re
A;Reference number: A55412; MUID:95142124; PMID:7836374
A;Accession: I38890
A;Molecule type: mRNA
A;Residues: 1-384 <KES>
A;Cross-references: EMBL:U16999; NID:g642012; PIDN:AAB06261.1; PID:g642013
A;Experimental source: placenta
R;Ishibashi, T.; Bottaro, D.P.; Michieli, P.; Kelley, C.A.; Aaronson, S.A.
J. Biol. Chem. 269, 29897-29902, 1994
A;Title: A novel dual specificity phosphatase induced by serum stimulation and heat s
A;Reference number: A55413; MUID:95050849; PMID:7961985
A;Accession: A55413
A;Molecule type: mRNA
A;Residues: 1-69, GLY-172-TYR, ILE-174-ILE, SER-176-ASP, ASP-178-ASP, ASP-180-ASP, GLY-182-ASP,
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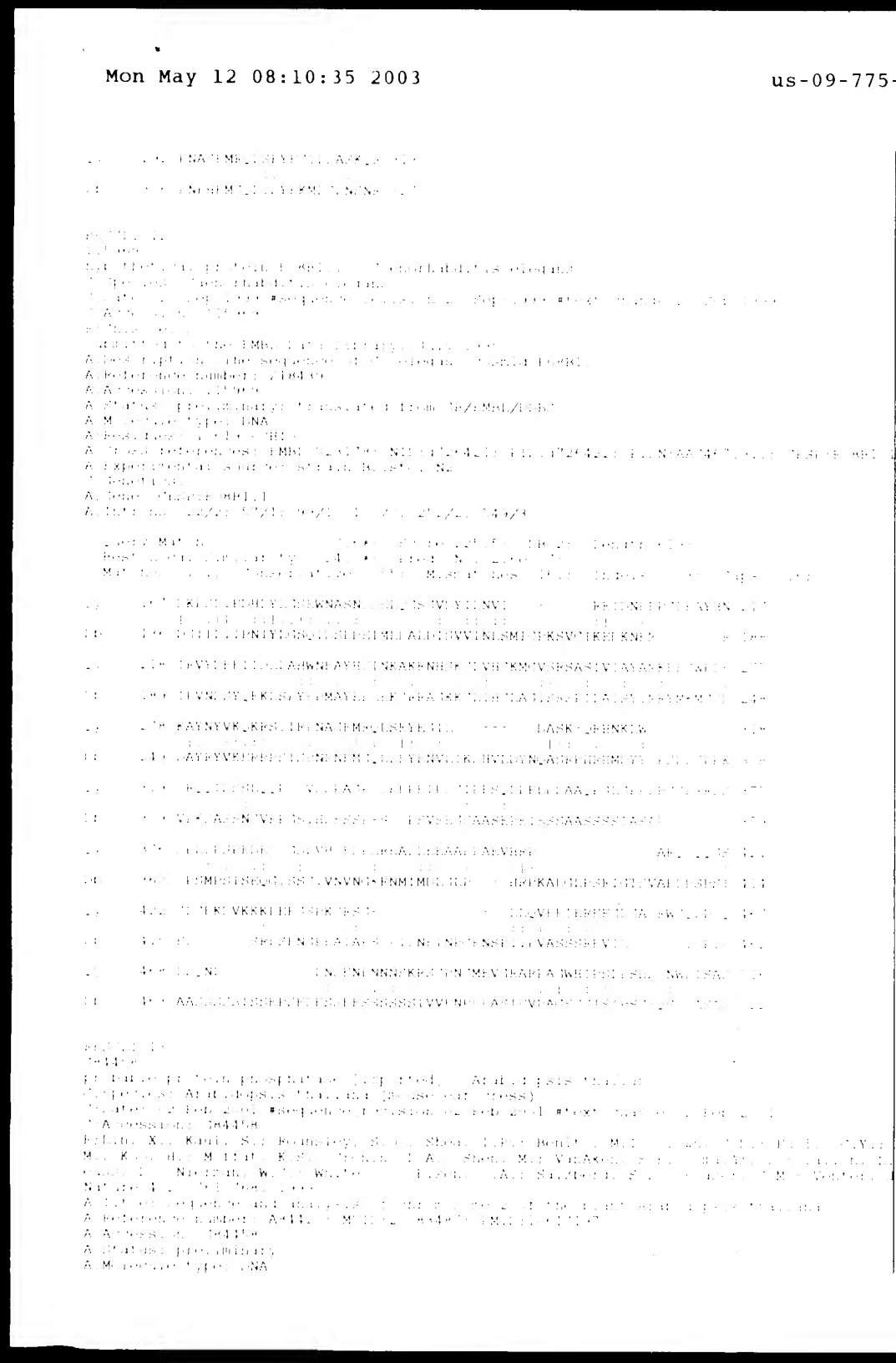

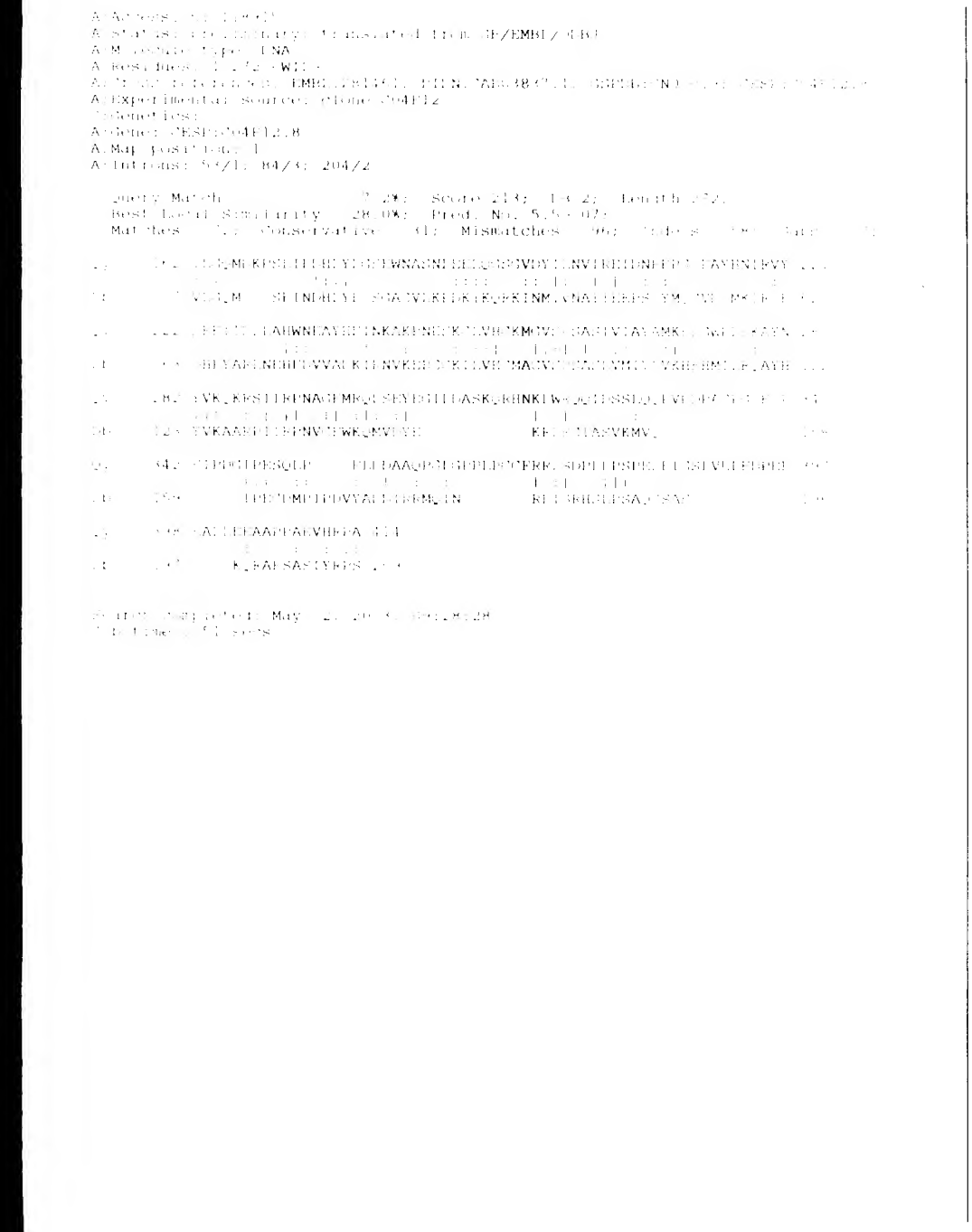

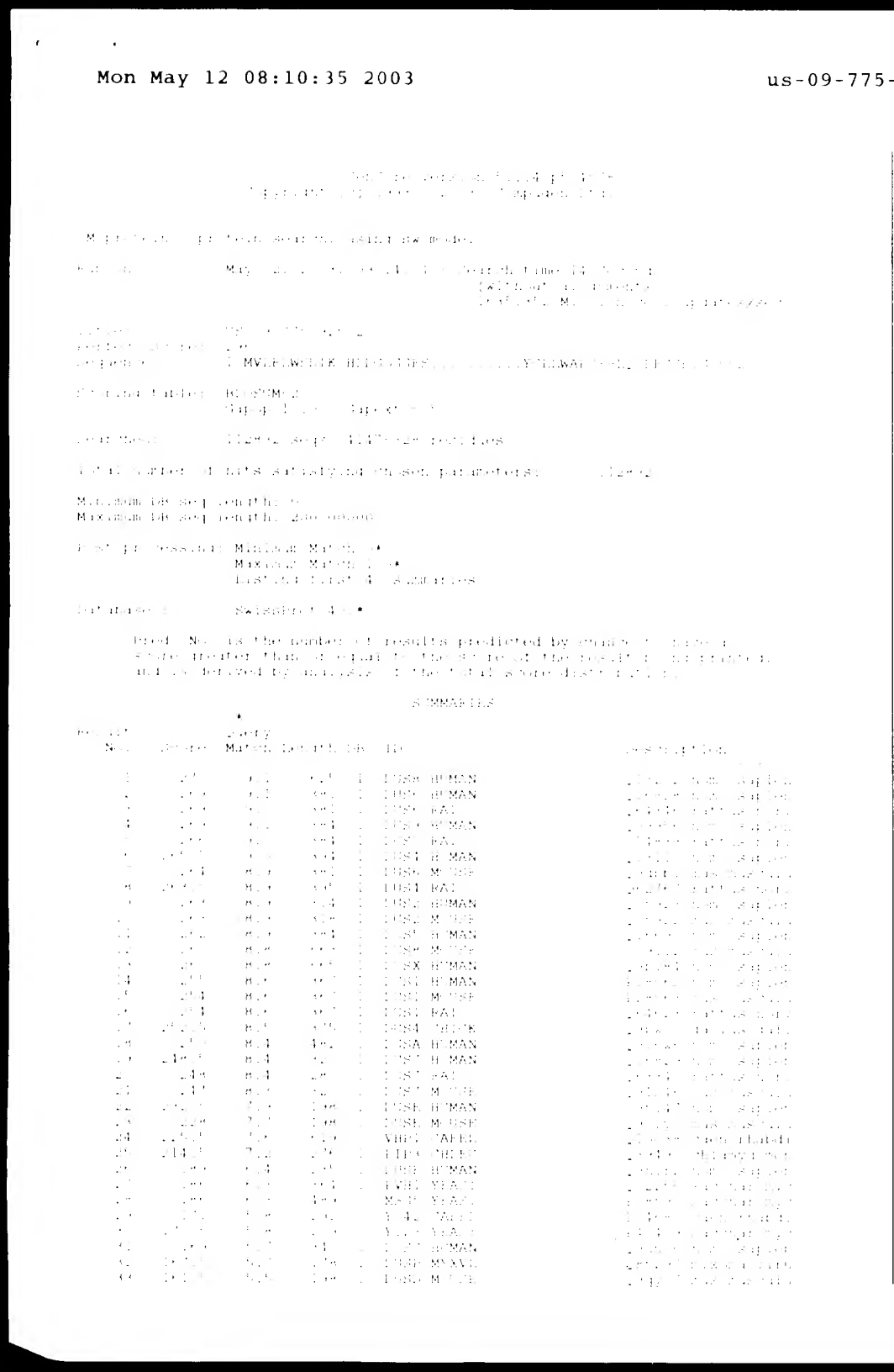

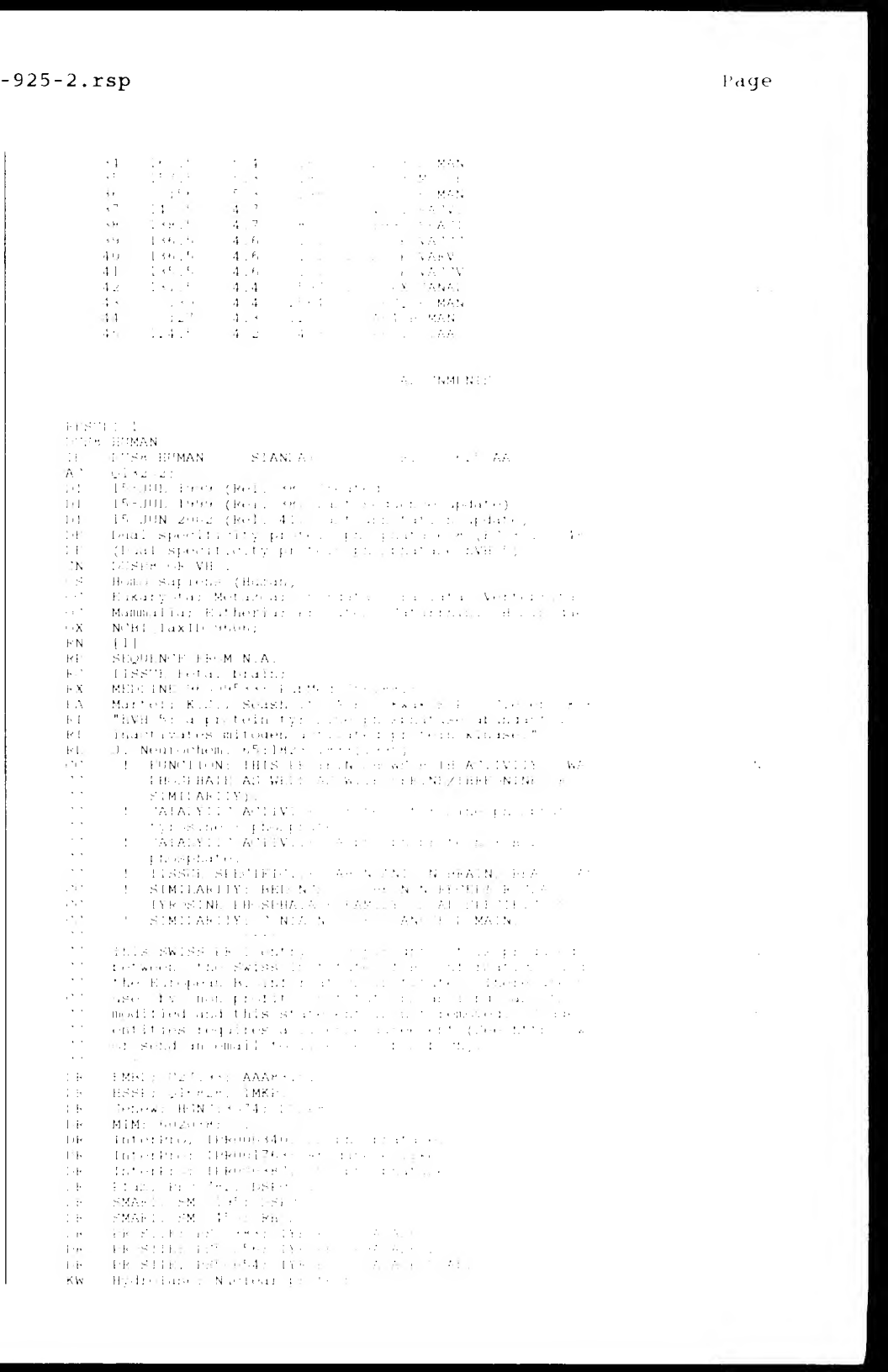

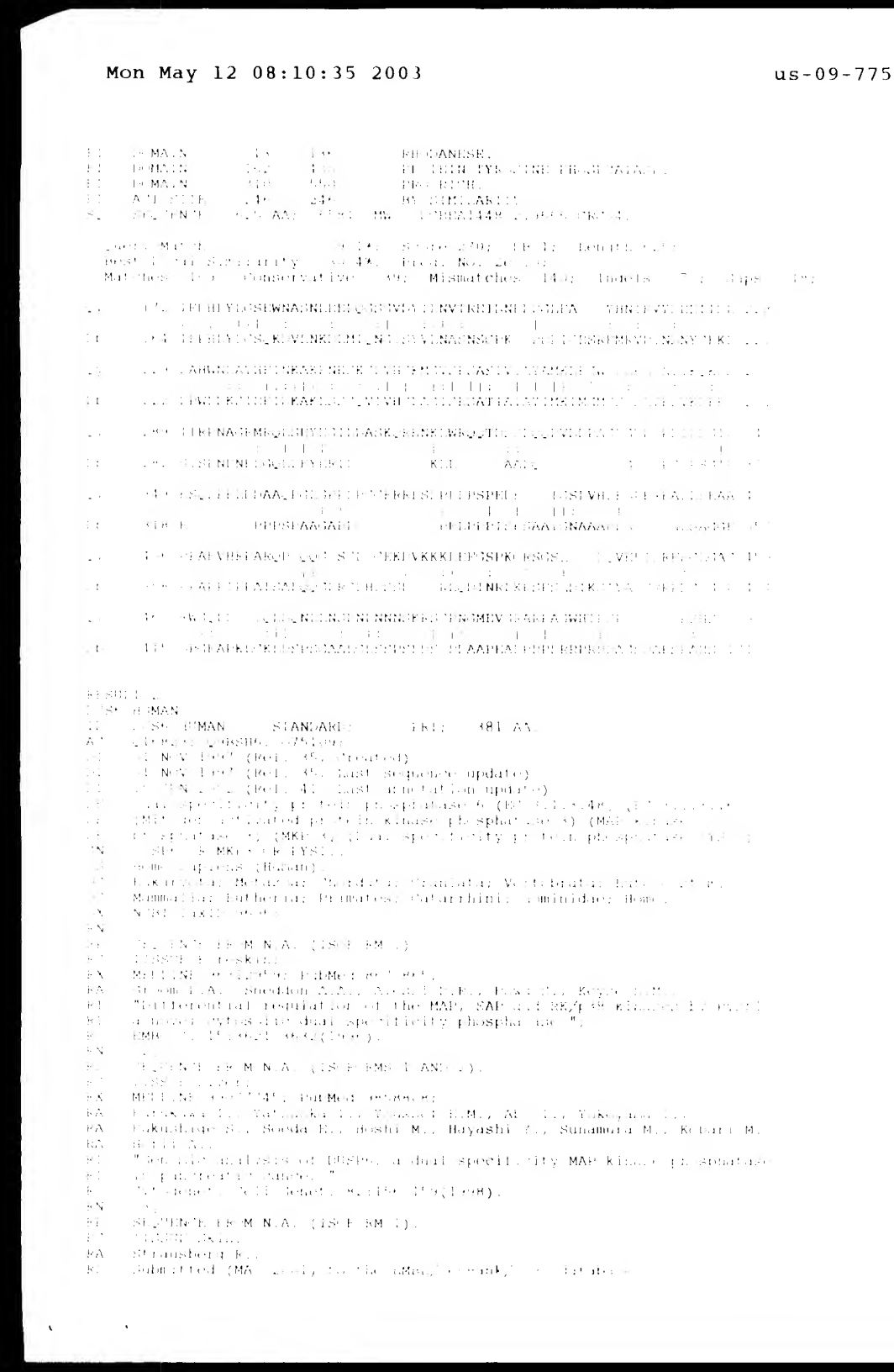

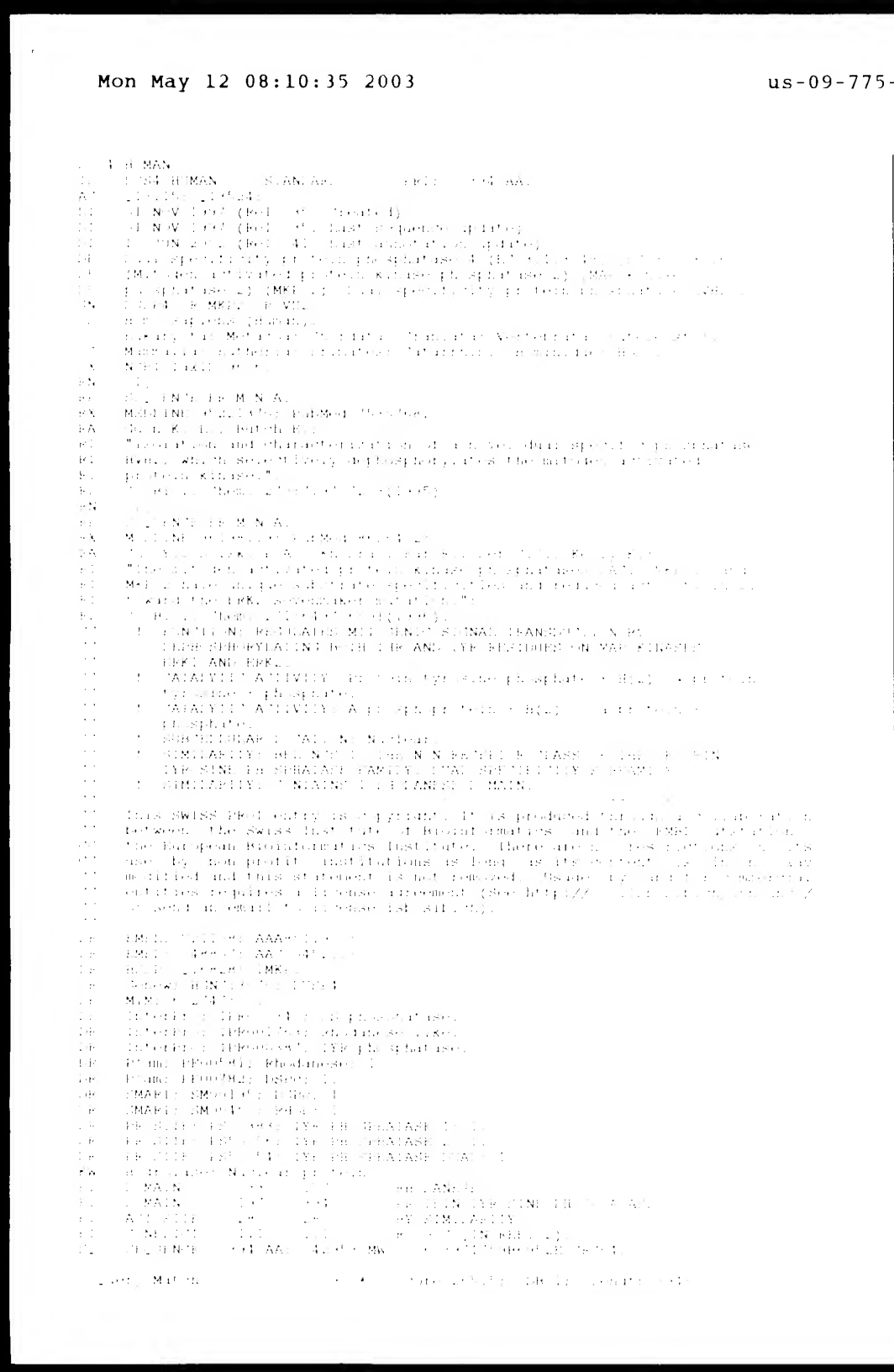

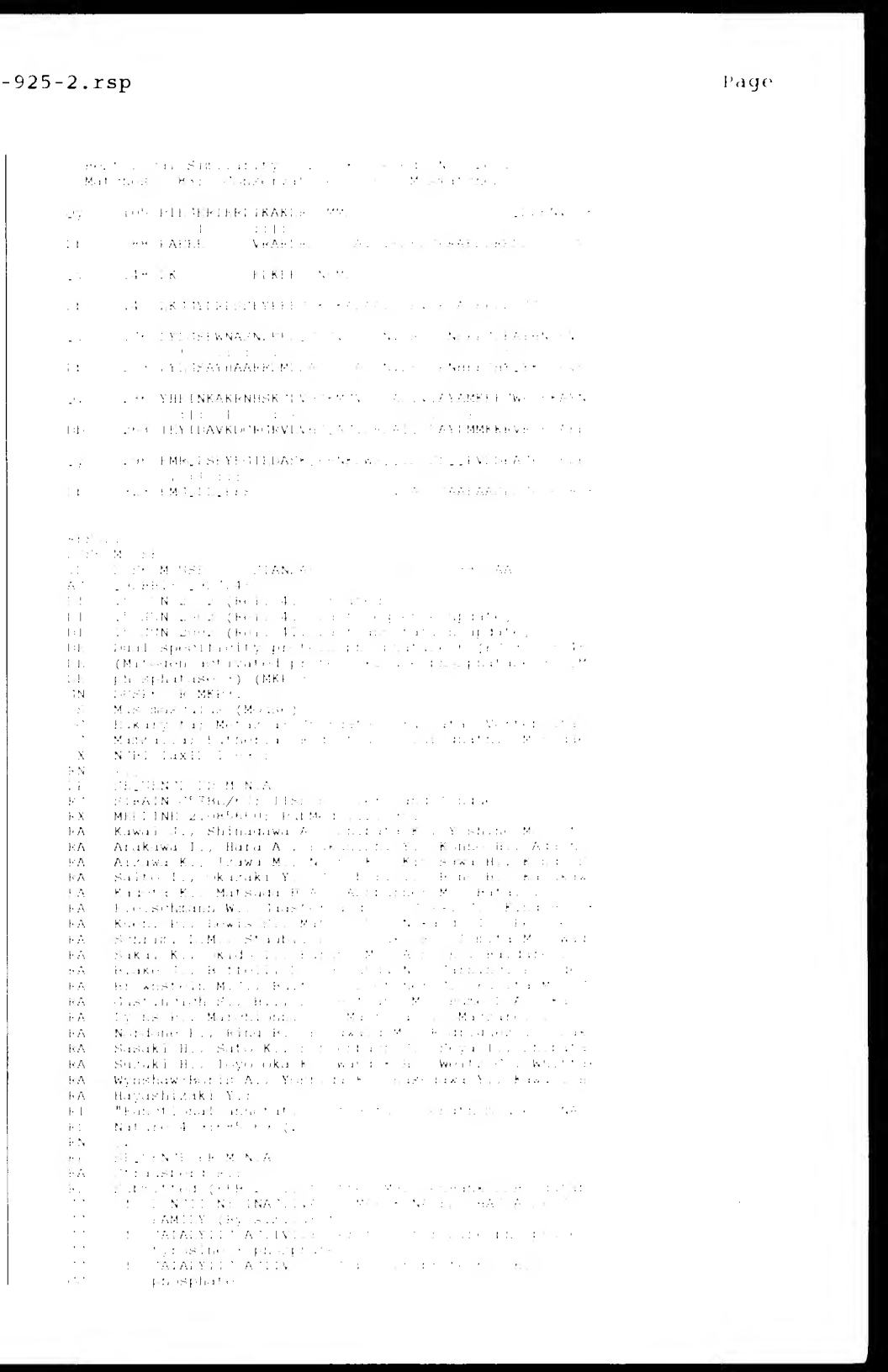

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CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AE[illegible]; BAB[illegible].1; -.
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DR   HSSP; Q16828; 1MKP.
DR   MGD; MGI:1914853; Dusp6.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; [illegible]; [illegible]; 1.
DR   SMART; [illegible]; [illegible]; 1.
DR   SMART; [illegible]; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase.
FT   DOMAIN       19    146       RHODANESE.
FT   DOMAIN      206    381       PROTEIN TYROSINE PHOSPHATASE.
FT   ACT_SITE    293    293       BY SIMILARITY.
FT   CONFLICT     22     22       W -> G (IN REF. 1; BAB[illegible]).
FT   CONFLICT     34     34       L -> I (IN REF. 1; BAB[illegible]).
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  Best Local Similarity   28.6%;  Pred. No. 2.4e-10;
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Qy        104 KPIEGERTERLIEAKL[illegible] 1[illegible]
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Qy        164 [illegible] 2[illegible]
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RESULT 8
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DT   1[illegible] 1996 (Rel. 3[illegible], Created)
DT   1[illegible] 1996 (Rel. 3[illegible], Last sequence update)
DT   1[illegible] JUN 200[illegible] (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Mitogen-activated protein kinase phosphatase 2) (MAP kinase
DE   phosphatase-2) (MKP-2).
GN   DUSP4 OR MKP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=95301550; PubMed=7782322;
RA   Misra-Press A., Rim C.S., Yao H., Roberson M.S., Stork P.J.S.;
RT   "A novel mitogen-activated protein kinase phosphatase. Structure,
RT   expression, and regulation.";
RL   J. Biol. Chem. 270:14587-14596(1995).
CC   -!- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
CC       DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
CC       ERK1 AND ERK2 (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- TISSUE SPECIFICITY: EXPRESSED AT MODERATE LEVELS IN NEARLY ALL
CC       TISSUES AND CELLS INCLUDING BRAIN, SPLEEN, AND TESTIS WITH THE
CC       HIGHER EXPRESSION IN THE HEART AND LUNG AND LOWER EXPRESSION IN
CC       SKELETAL MUSCLE AND KIDNEY. UNDETECTABLE IN LIVER. EXPRESSED IN
CC       MANY AREAS OF THE BRAIN WITH VERY STRONG EXPRESSION IN THE
CC       HIPPOCAMPUS, PIRIFORM CORTEX, AND THE SUPRACHIASMATIC NUCLEUS.
CC   -!- INDUCTION: BY MITOGENS AND BY STRESS.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U23438; AAC52491.1; -.
DR   HSSP; Q16828; 1MKP.
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DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00581; Rhodanese; 1.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Nuclear protein.
FT   DOMAIN       34    158       RHODANESE.
FT   DOMAIN      198    [illegible]       PROTEIN TYROSINE PHOSPHATASE.
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SQ   SEQUENCE   395 AA;  [illegible] MW;  A36EFF[illegible]78A050FD CRC64;

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  Best Local Similarity   28.7%;  Pred. No. 2.8e-10;
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Db         [illegible] FALLE      VKAKEKSGLYSAVIVYDEKSPKAE[illegible] 14[illegible]

Qy        148 LK          ELKEFTD              NEMLLL         LQ[illegible]MDKE[illegible] 175
Db        [illegible] 2[illegible]

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Qy        2[illegible] 2[illegible]
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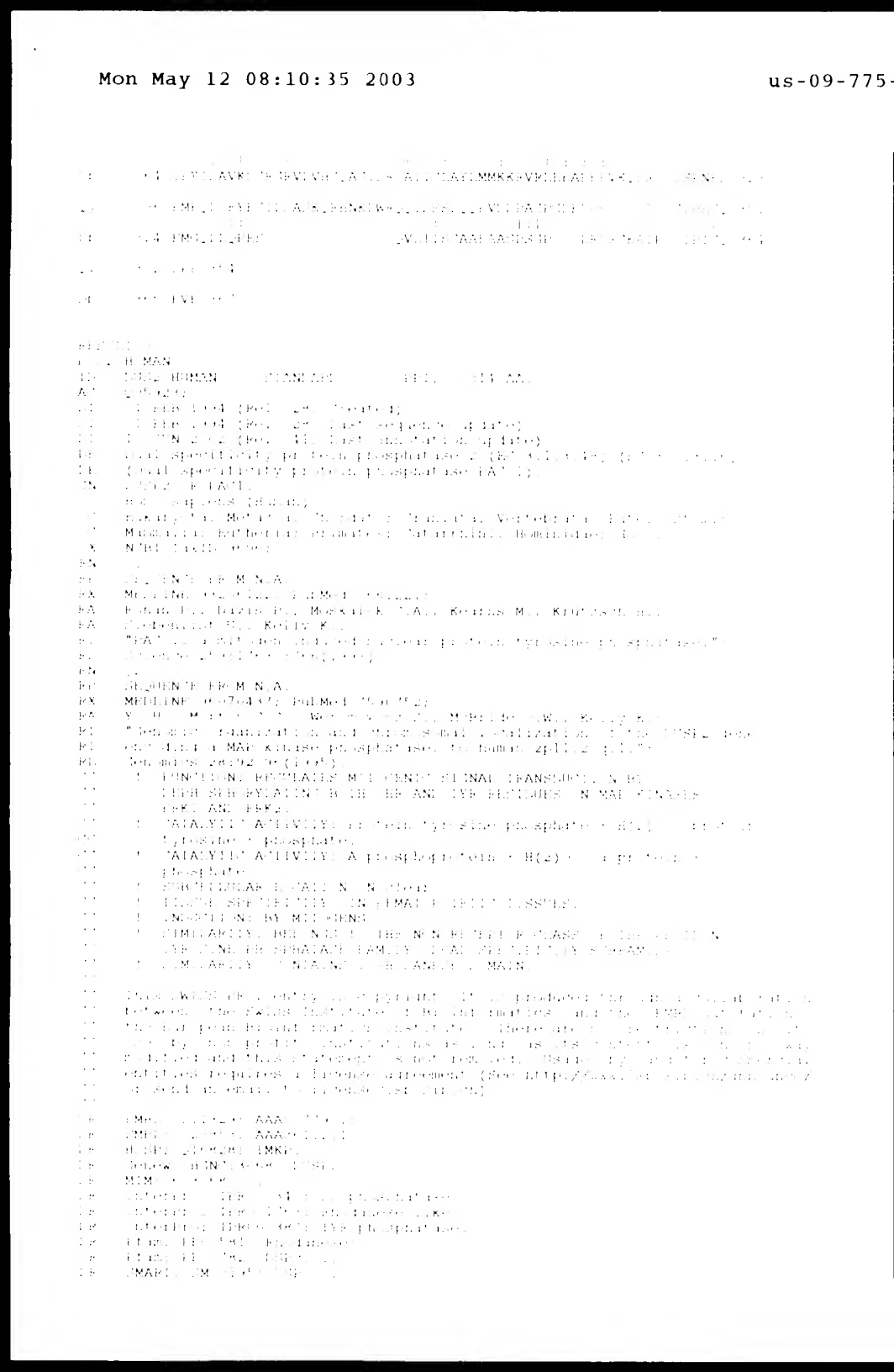

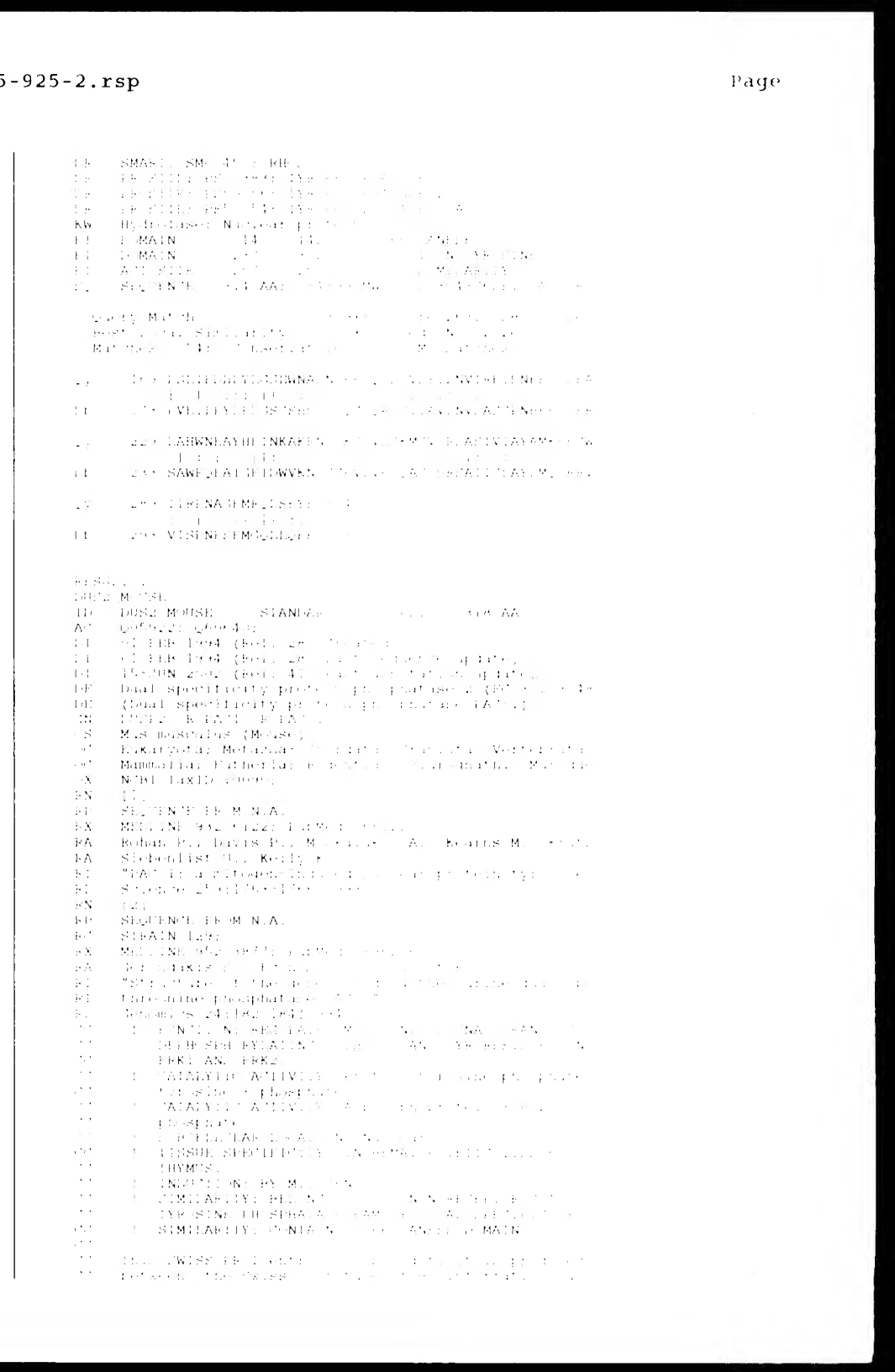

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DR PDB; 1YWF; 15-MAR-04.
DR PFAM; PF00782; DSPc; 1.
DR SMART; SM00195; DSPc; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase; Nuclear protein; Alternative splicing.
FT DOMAIN 29 129 PHOSPHATASE.
FT DOMAIN 241 360 PROTEIN-TYROSINE/DUAL-SPECIFICITY
FT ACT_SITE 261 261 BY SIMILARITY.
FT VARSPLIC 175 179 QCPVE -> VSSHL (IN SHORT FORM).
FT VARSPLIC 340 418 MISSING (IN SHORT FORM).
FT CONFLICT 31 32 PI -> WL (IN REF. 2).
FT CONFLICT 49 - A -> V (IN REF. 2).
FT CONFLICT 156 156 I -> A (IN REF. 2).
SQ SEQUENCE 418 AA; 47510 MW; A2D9A1B9DF5C7D41 CRC64;

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Best Local Similarity 51.8%; Pred. No. 2.2e-11;
Matches 58; Conservative 29; Mismatches 66; Indels 16; Gaps 3;

ID DUS5_HUMAN
AC Q16828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2004 (Rel. 43, Last annotation update)
DE Dual specificity protein phosphatase 5 (EC 3.1.3.48) (EC 3.1.3.16).
DE Class specificity protein phosphatase hVH5.
GN DUSP5 OR VH5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95050844; PubMed=7961985;
RA Ishibashi T., Bottaro D.P., Michieli P., Kelley C.A.,
RA Aaronson S.A.;
RT "A novel dual specificity phosphatase induced by serum stimulation
RT and heat shock.";
RL J. Biol. Chem. 269:29897-29902(1994).
RN [2]
RP REVISIONS.
RA Bottaro D.P.;
RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: HYDROLYZES EFFICIENTLY ACTIVATED MAP KINASES ERK1 AND
CC ERK2 BUT NOT JNK1 OR P38. THE HIGHEST RELATIVE ACTIVITY IS TOWARD ERK1.
CC -!- CATALYTIC ACTIVITY: Protein-tyrosine phosphate + H(2)O = protein-
CC tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS 1 SUBFAMILY OF PROTEIN
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 PHOSPHATASE DOMAIN.
CC -!-
CC -!- This SWISS-PROT entry is copyrighted. It is produced through a
CC collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -!-
DR EMBL; L12540; AAA19600.1; -.
DR EMBL; X76358; AAA85140.1; -.
DR PDB; 1YWE; 15-MAR-04.
DR PDB; 1YWF; 15-MAR-04.
DR PFAM; PF00782; DSPc; 1.
DR SMART; SM00195; DSPc; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase; Nuclear protein.
FT DOMAIN 7 129 PHOSPHATASE.
FT DOMAIN 190 384 PROTEIN-TYROSINE/DUAL-SPECIFICITY
FT DOMAIN 54 74 NUCLEAR LOCALIZATION SIGNAL (BIPARTITE)
FT DOMAIN 79 82 POLY-GLY.
FT ACT_SITE 263 263 BY SIMILARITY.
FT CONFLICT 9 11 PQL -> GHV (IN REF. 2).
FT CONFLICT 71 73 A -> P (IN REF. 2).
FT CONFLICT 195 196 AR -> P (IN REF. 2).
SQ SEQUENCE 484 AA; 54237 MW; D2B726F7C0414306 CRC64;

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Best Local Similarity 51.8%; Pred. No. 2.2e-11;
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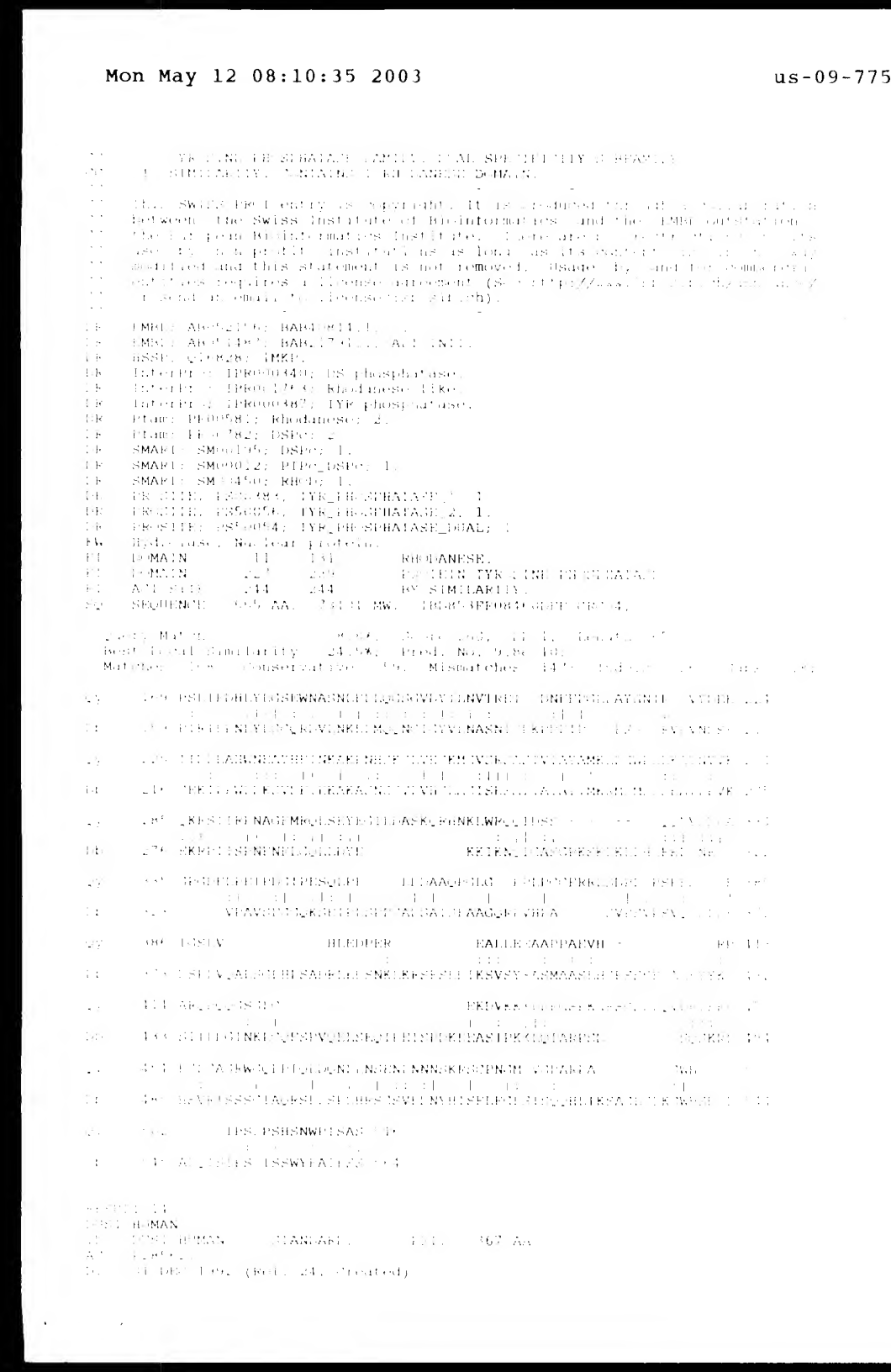

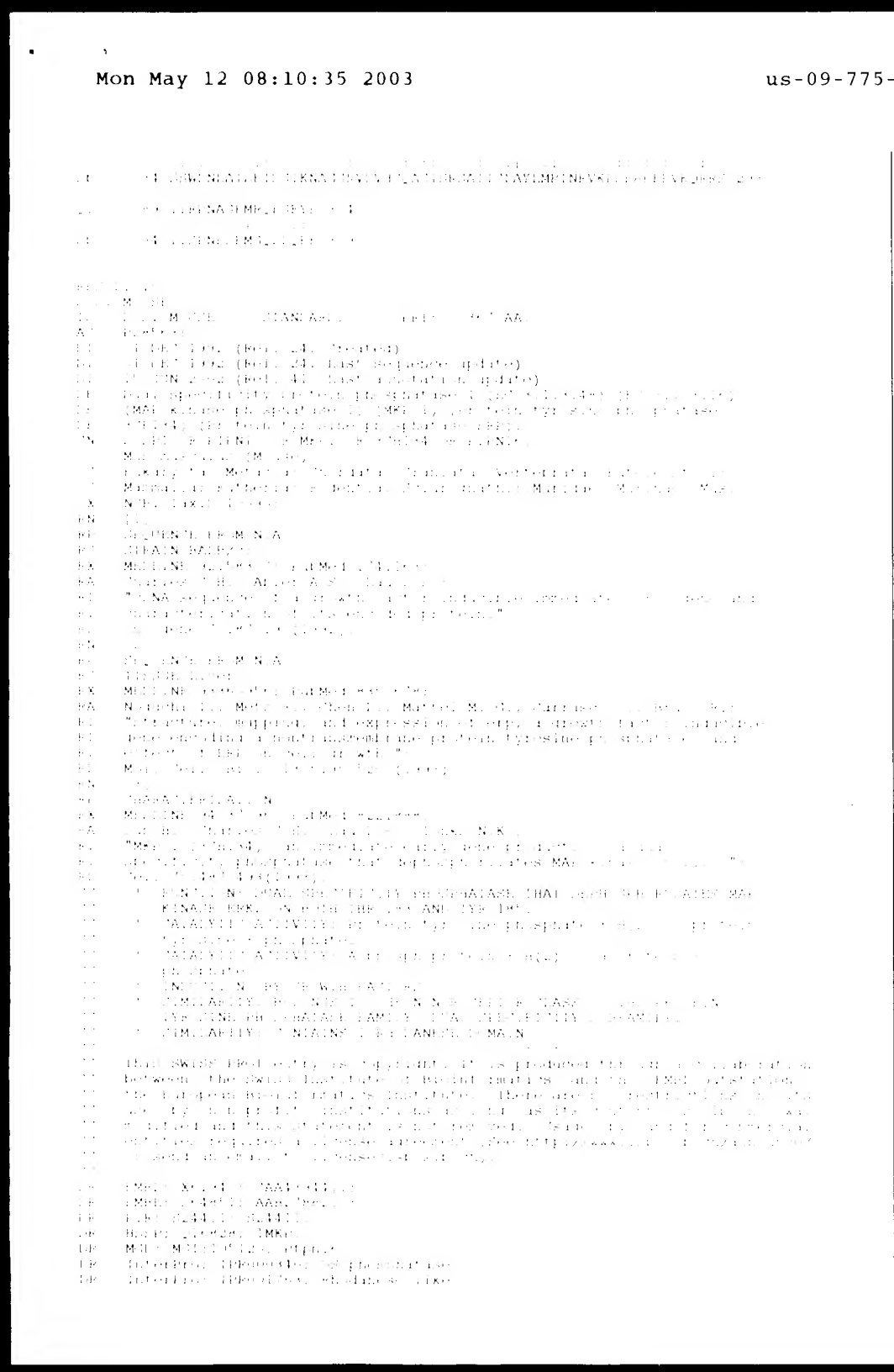

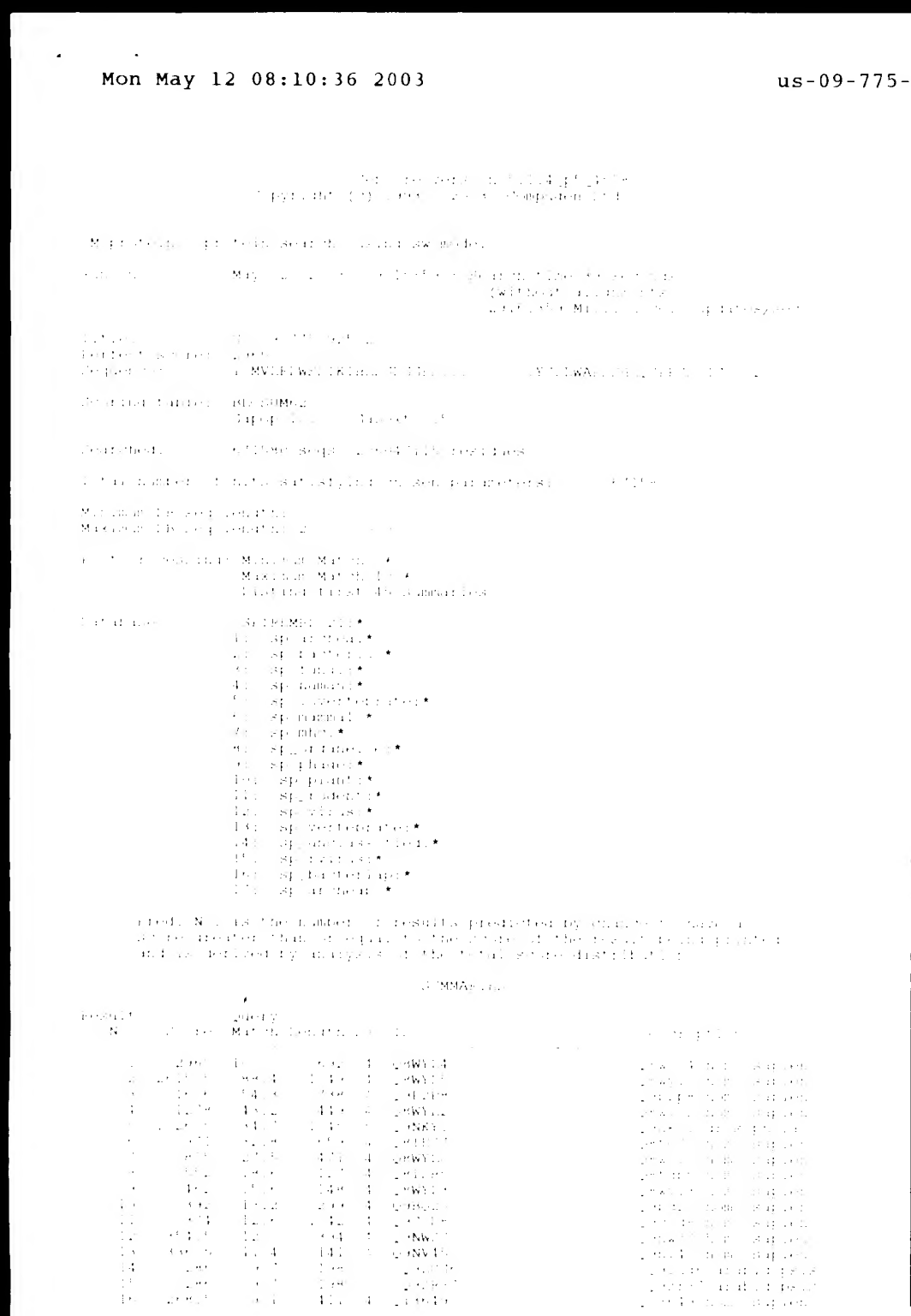

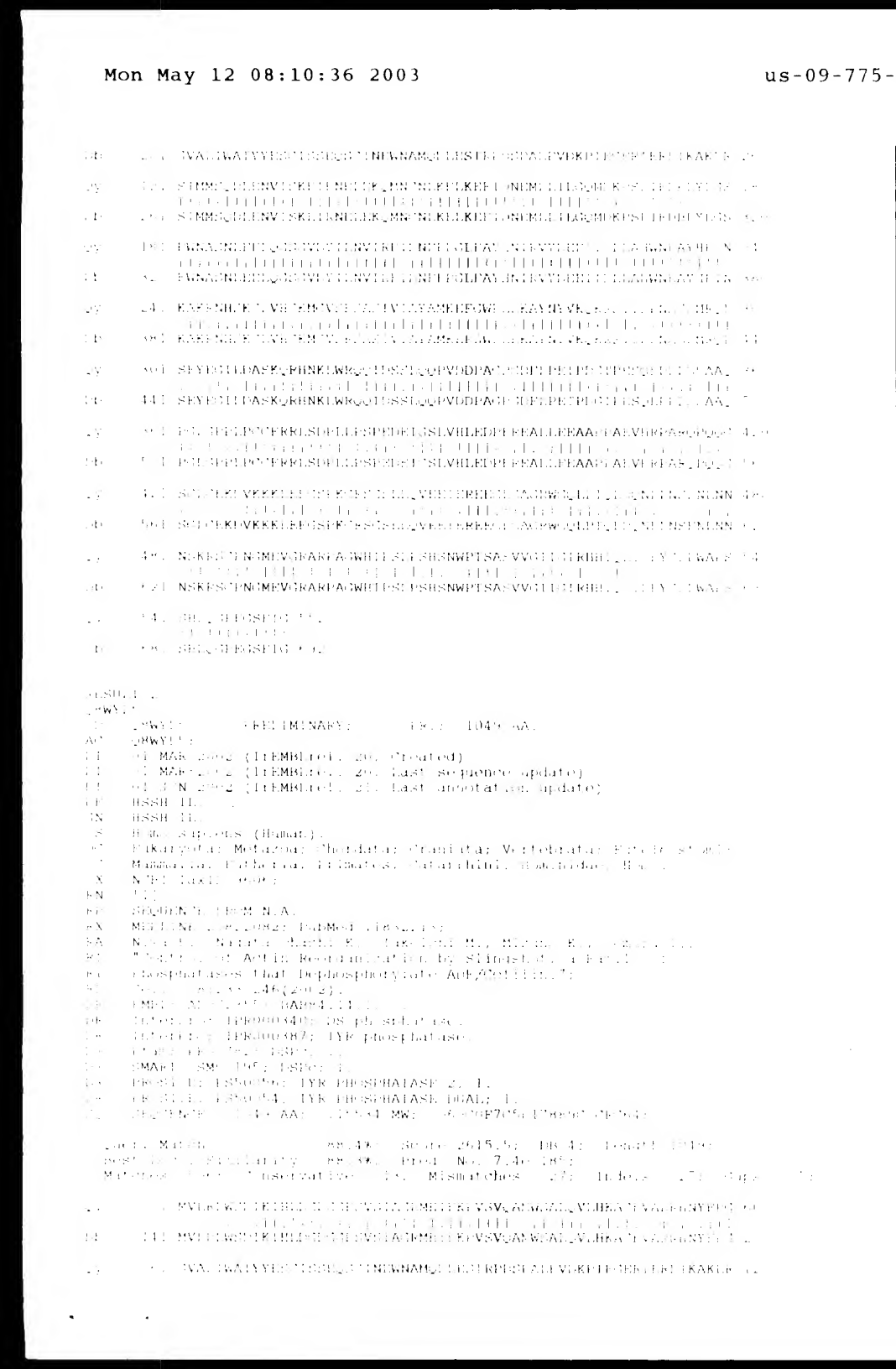

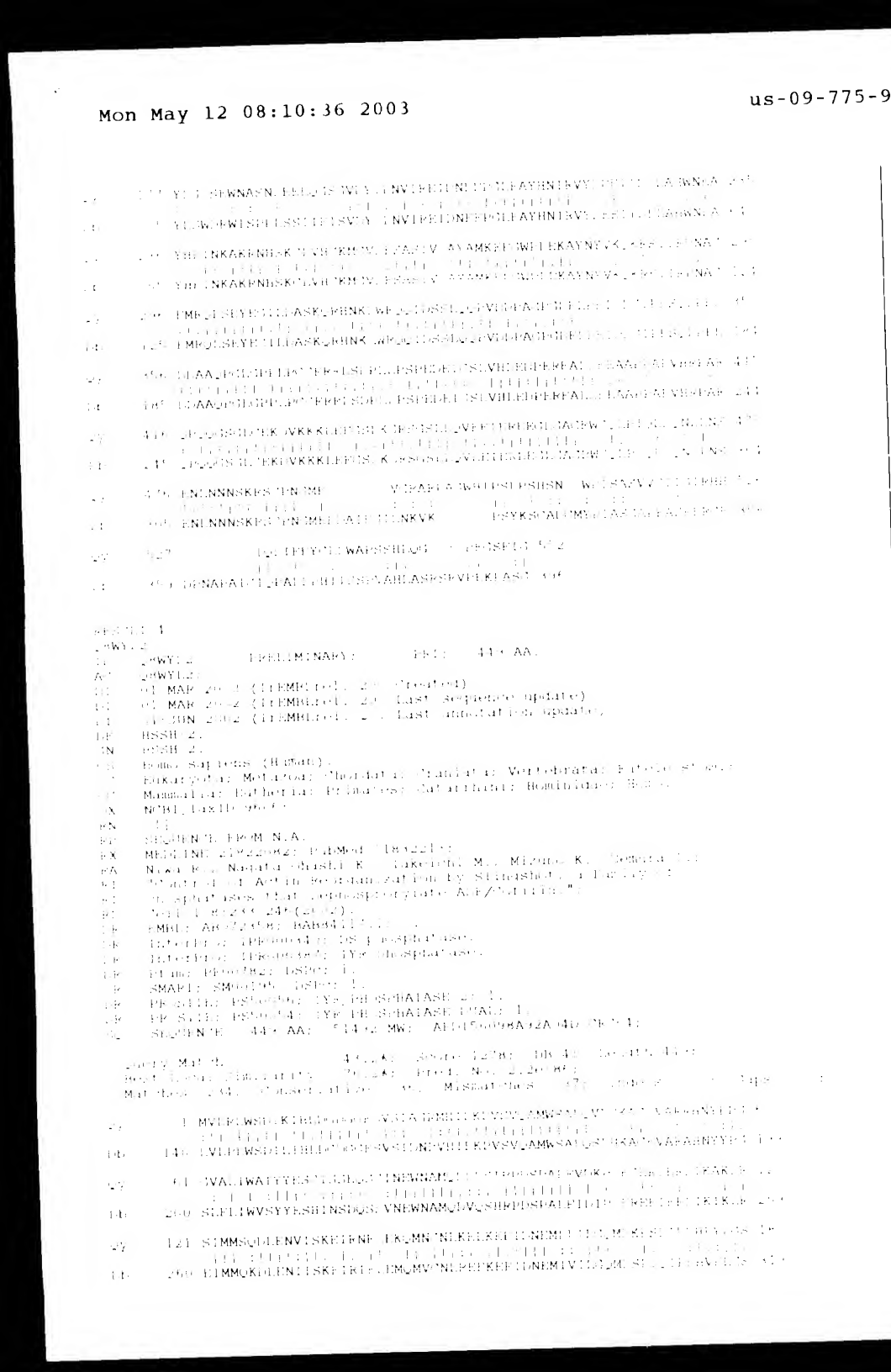

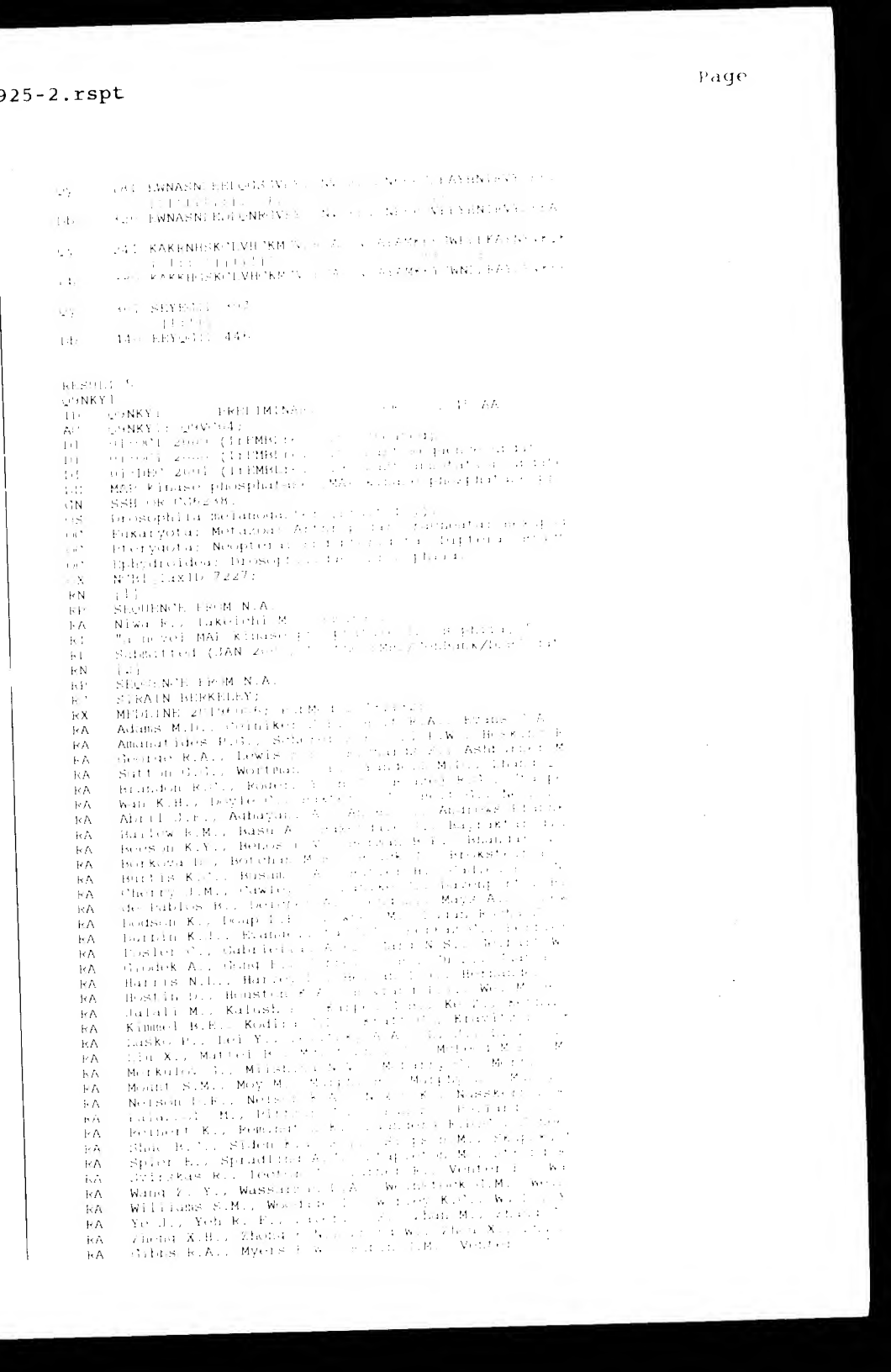

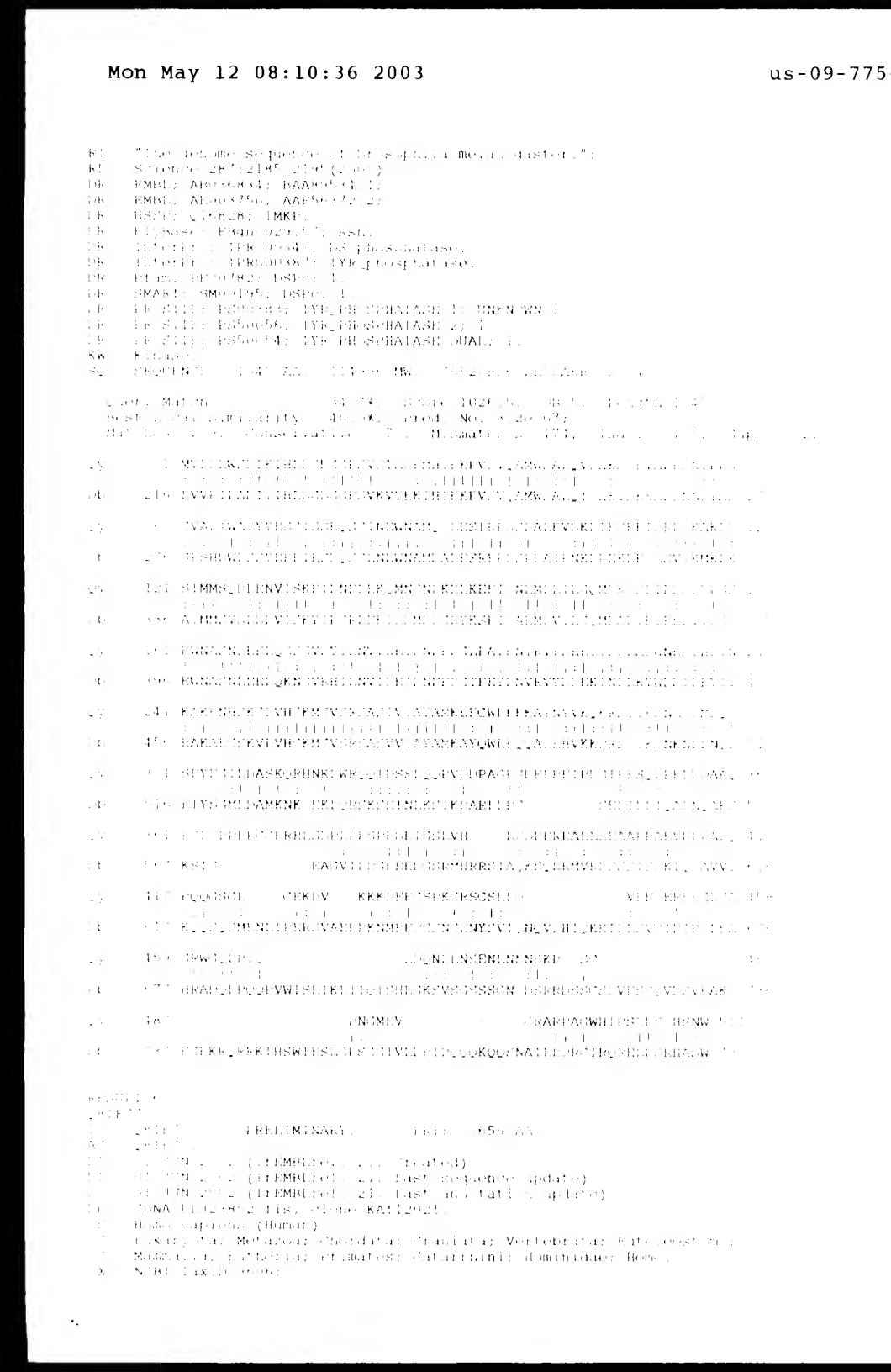

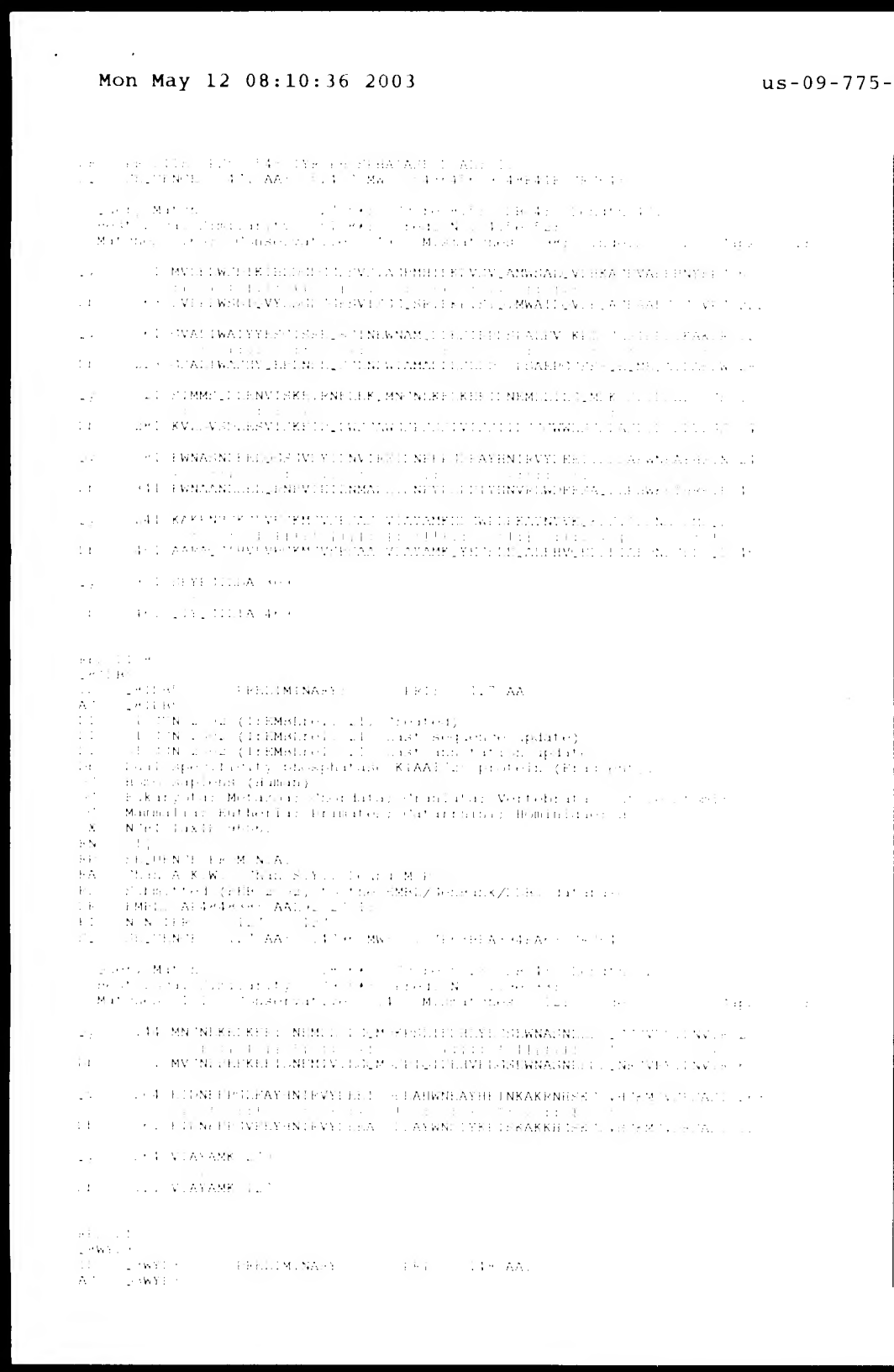

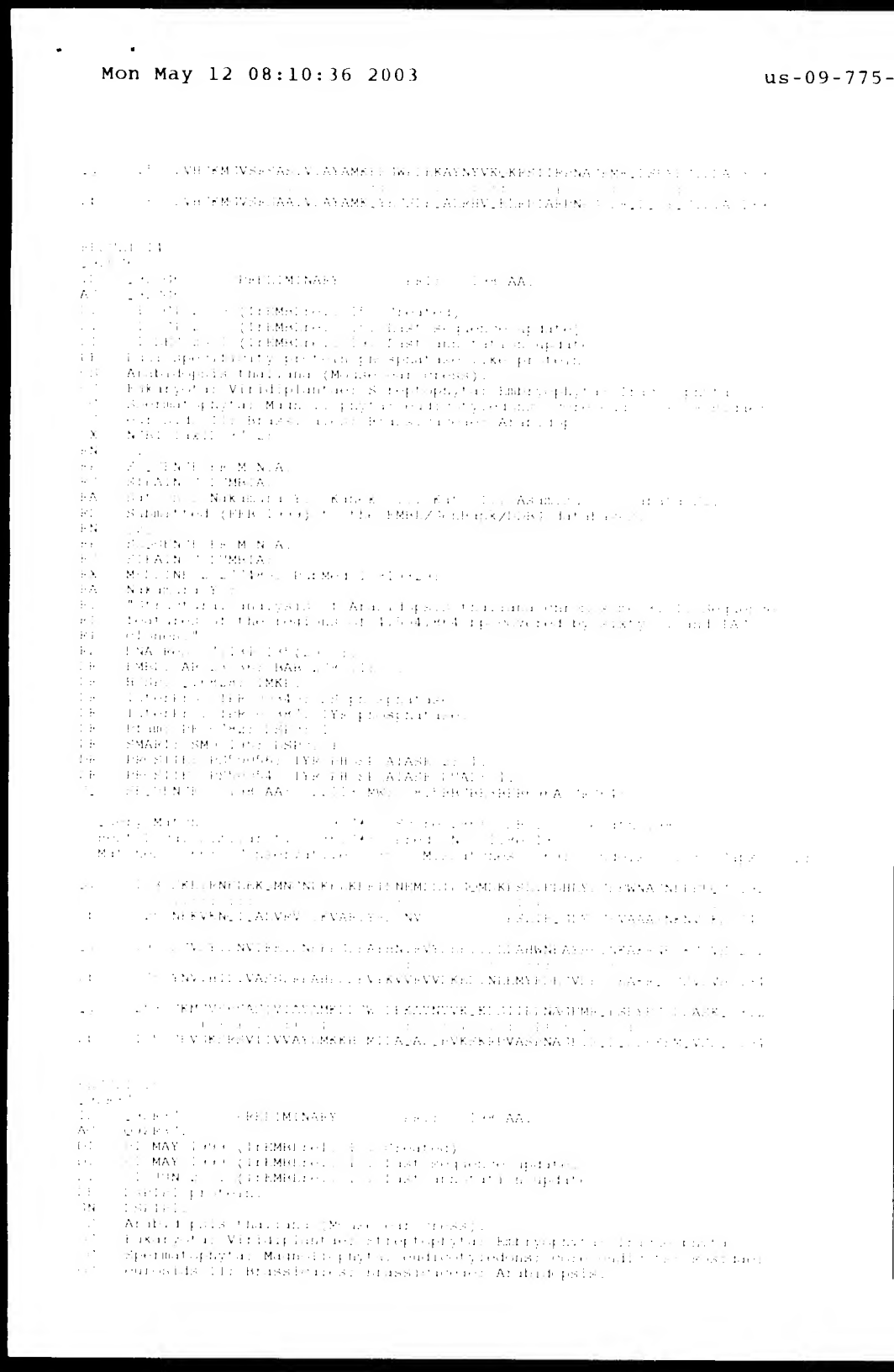

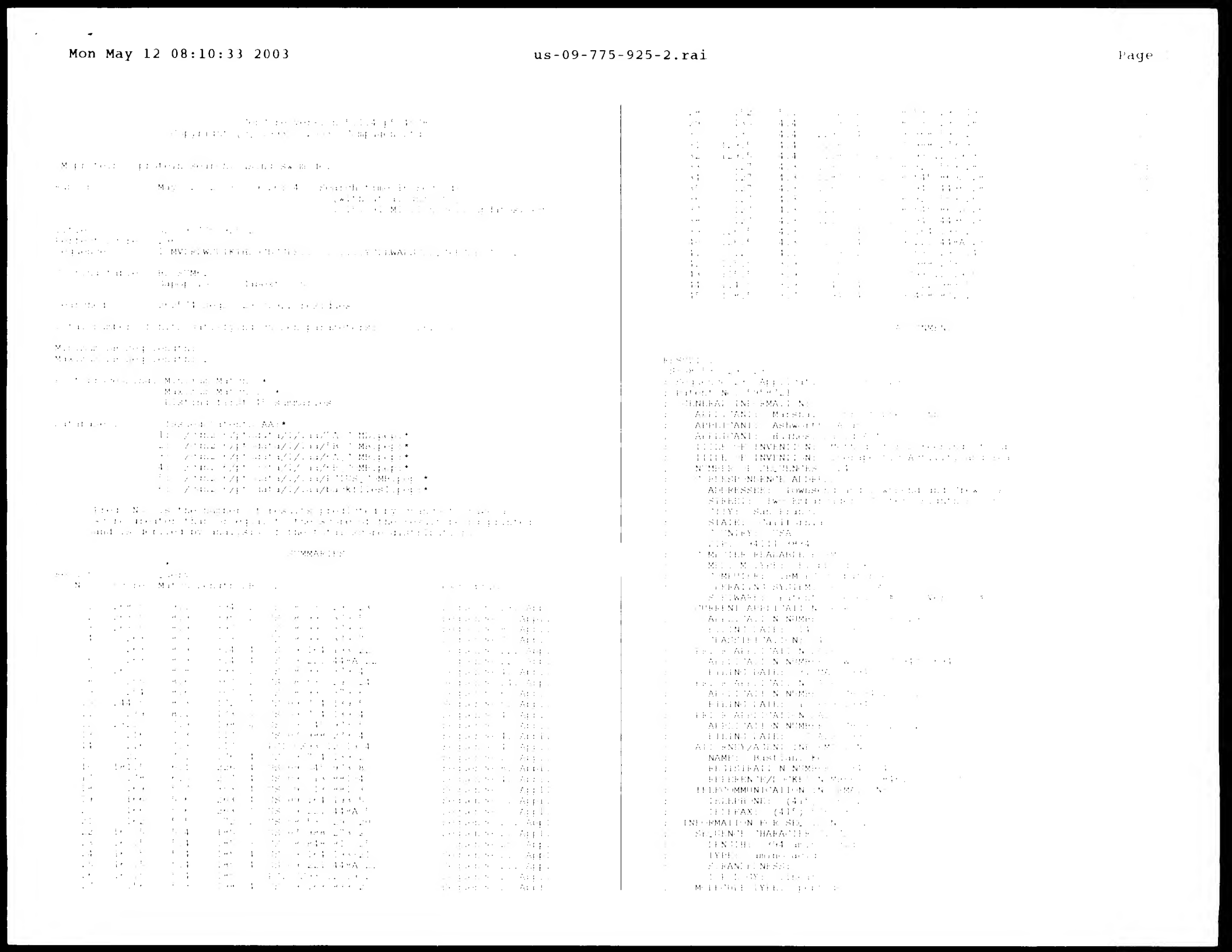

TELEPHONE: (202)672-5569
TELEFAX: (202)672-5399
TELEX: 89-1233

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

US-09-775-925-2

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Best Local Similarity 98.8%; Pred. No. 1.6e-12;
Matches 44; Conservative 2; Mismatches 48; Indels 0; Gaps 0;

Qy 1 MGSIVYYLNVTRETCNFTCLEAYSNETVTVEYVTTTWKTRVYNYKAKGSRCSIWR 57

Db 2 MDALGYALNVVAKTGGLFDSIGHGVKDVATSIWNFVSTFQSGGASIAFSLVTIAL 58

RESULT 5
US-09-704-139-2
; Sequence 2, Application US/09704139
; Patent No. 6420134
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosanna
; TITLE OF INVENTION: Ras-p21 A NOVEL DUAL SPECIFICITY PHOSPHATASE AND ITS USES THEREFOR
; FILE REFERENCE: 10448-018US1
; CURRENT APPLICATION NUMBER: US/09/704,139
; CURRENT FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: US 60/163,722
; PRIOR FILING DATE: 1999-02-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1390)
; OTHER INFORMATION: X, Xaa, Y, Q, or C
US-09-704-139-2

Query Match 7.1%; Score 210; DB 4; Length 176;
Best Local Similarity 48.0%; Pred. No. 1.1e-11;
Matches 54; Conservative 17; Mismatches 62; Indels 2; Gaps 2;

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Db 29 LFEGSARAAAALQAGVAVLVSAAGGPPRAAVLGVALVEVPEVPAGLGAHLED 84

Qy 237 ATHEIRKAEENGLA-VSESAEVCLGGLGIVIAVAMALSWGTEKAYNTVKSKFSFVAENE 295

Db 85 VAAEGAAAAAAAAAVSLSRVGRLDGHDLLLDAPSGPVKSAFTVAENE 131

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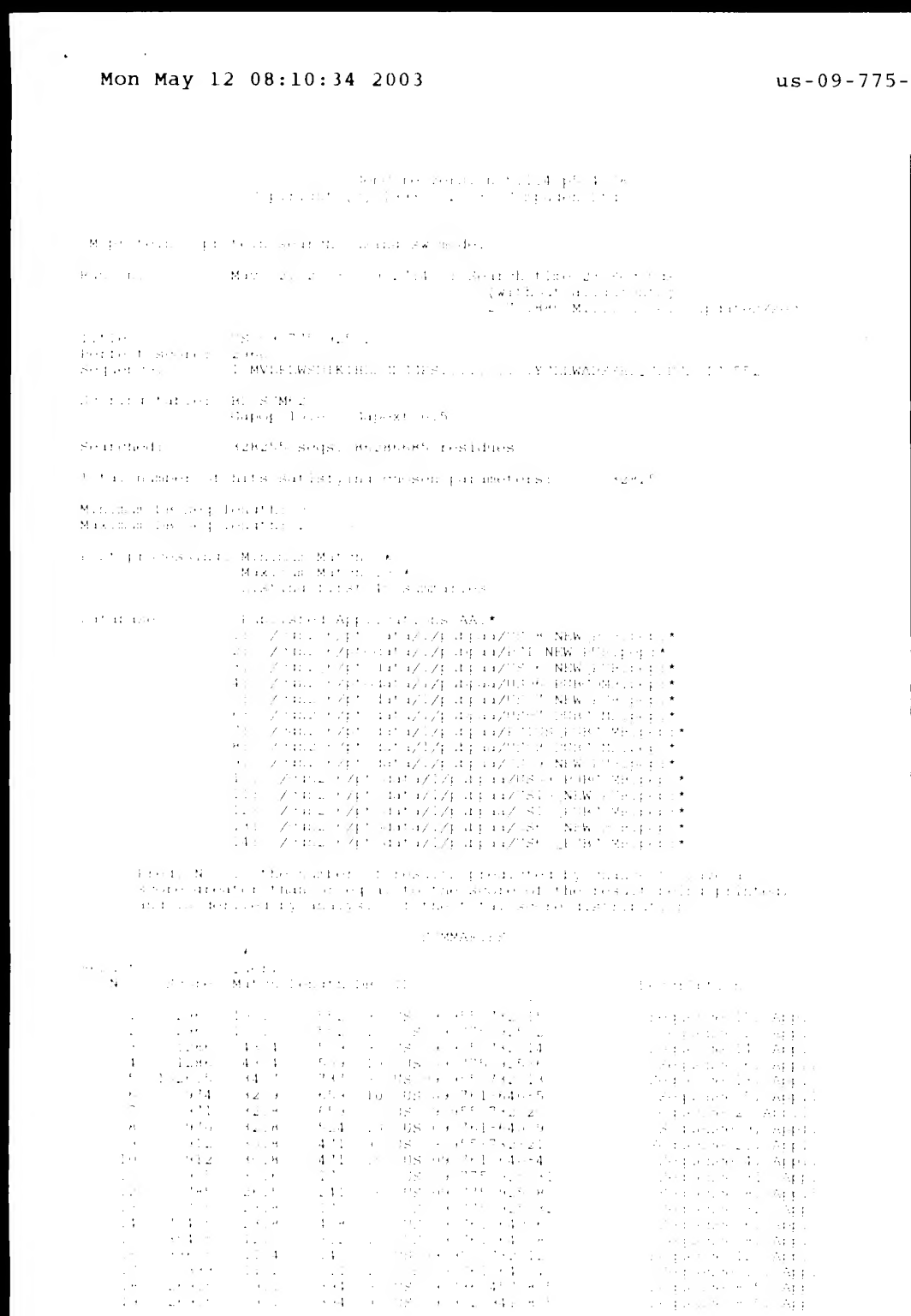
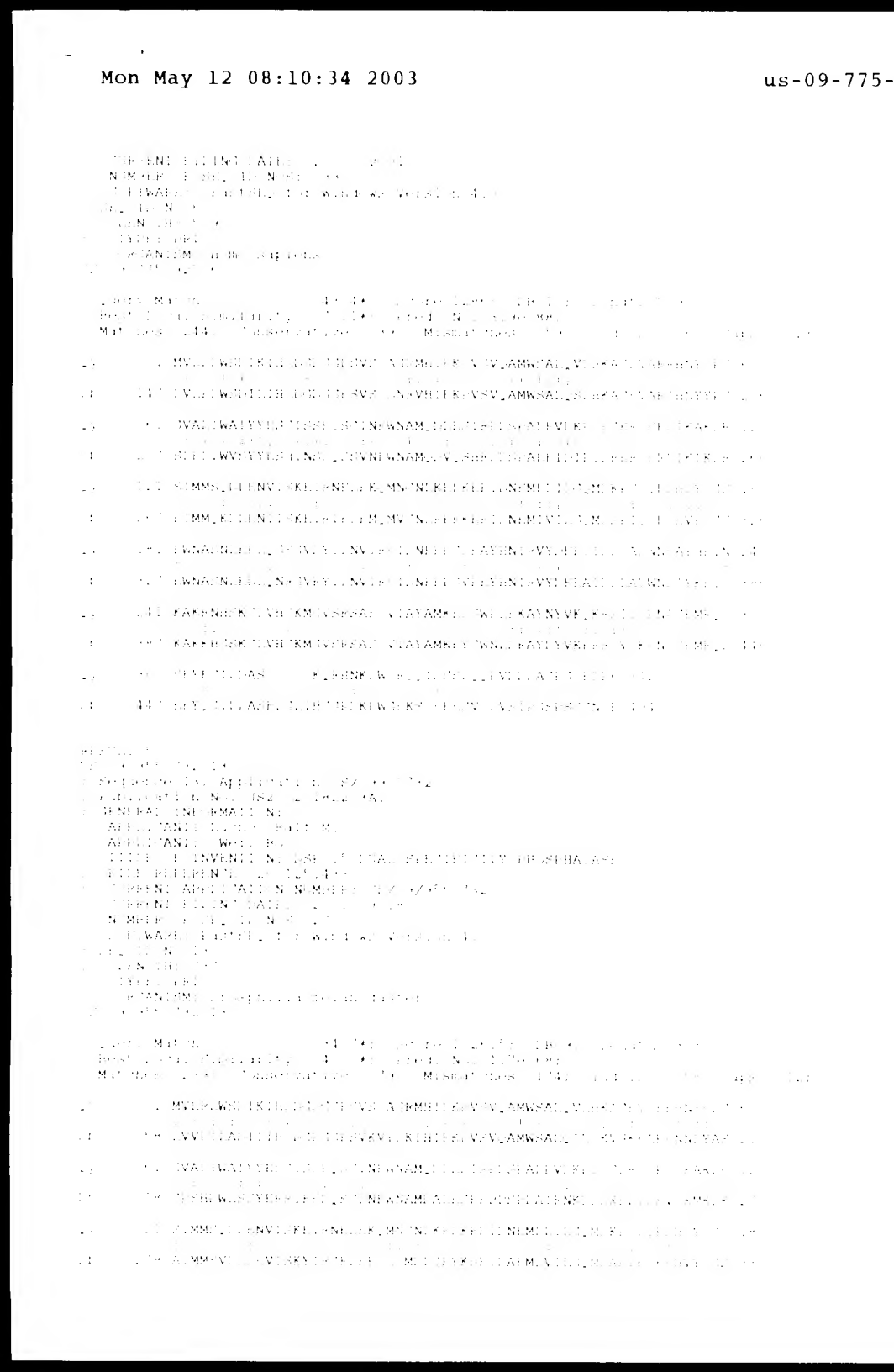
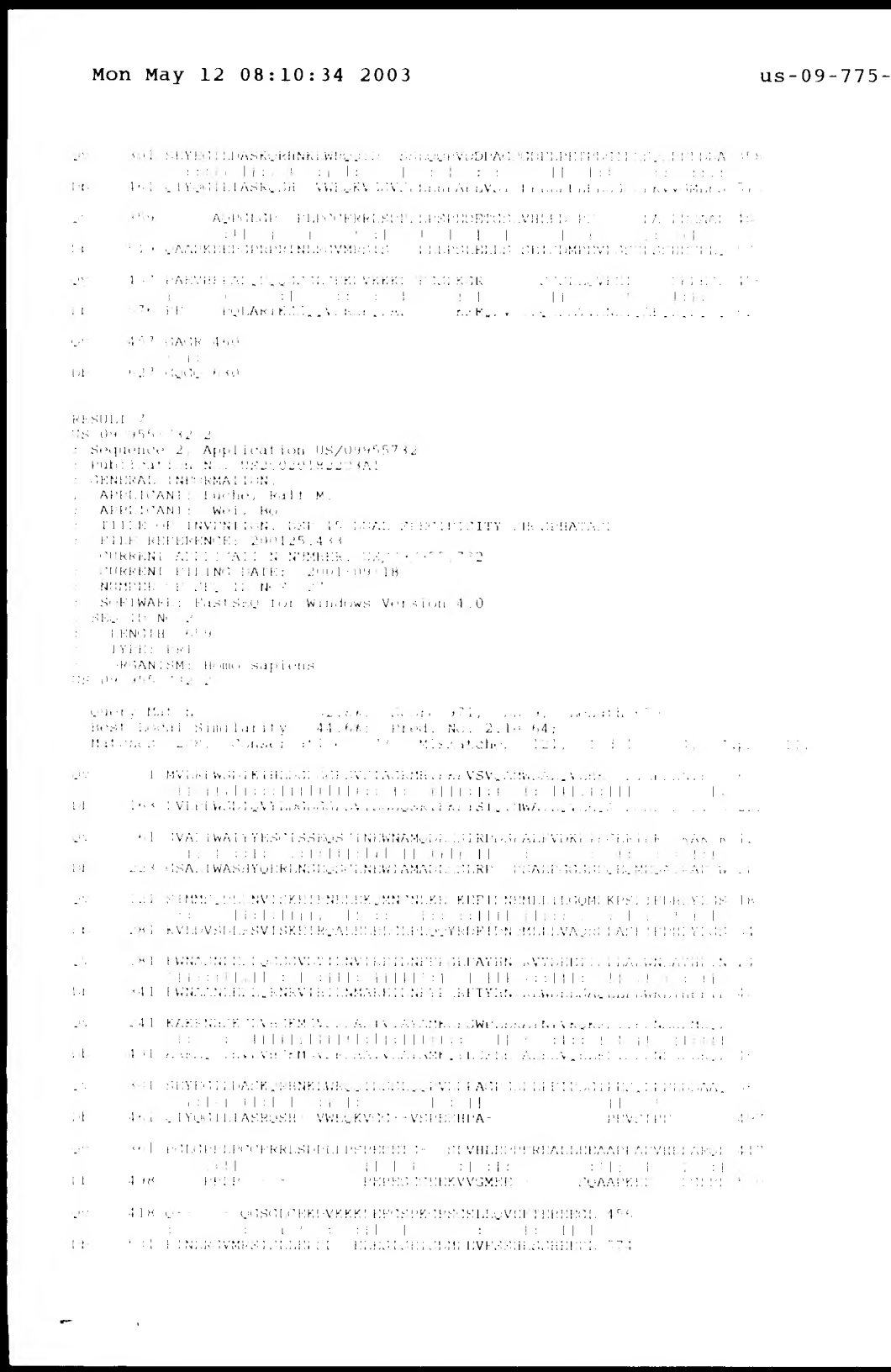
Search completed: May 12, 2003, 09:28:50
Job time : 18 secs







RESULT 8
US-09-761-640-9
; Sequence 9, Application US/09761640
; Patent No. US20020137042A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000964 CIP
; CURRENT APPLICATION NUMBER: US/09/761,640
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-761-640-9

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RESULT 2
US-09-095-732-2
; Sequence 2, Application US/09095732
; Publication No. US20020019022A1
; GENERAL INFORMATION:
; APPLICANT: Tucho, Karl M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: [illegible]
; FILE REFERENCE: 20025.433
; CURRENT APPLICATION NUMBER: US/09/095,732
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-095-732-2

Query Match 44.6%; Score 820; DB 10; Length 459;
Best Local Similarity 44.6%; Pred. No. 2.1e-64;
Matches 185; Conservative 46; Mismatches 121; Indels 0; Gaps 0;

RESULT 9
US-09-095-732-21
; Sequence 21, Application US/09095732
; Publication No. US20020168220A1
; GENERAL INFORMATION:
; APPLICANT: Tucho, Karl M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: [illegible]
; FILE REFERENCE: 20025.433
; CURRENT APPLICATION NUMBER: US/09/095,732
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-095-732-21

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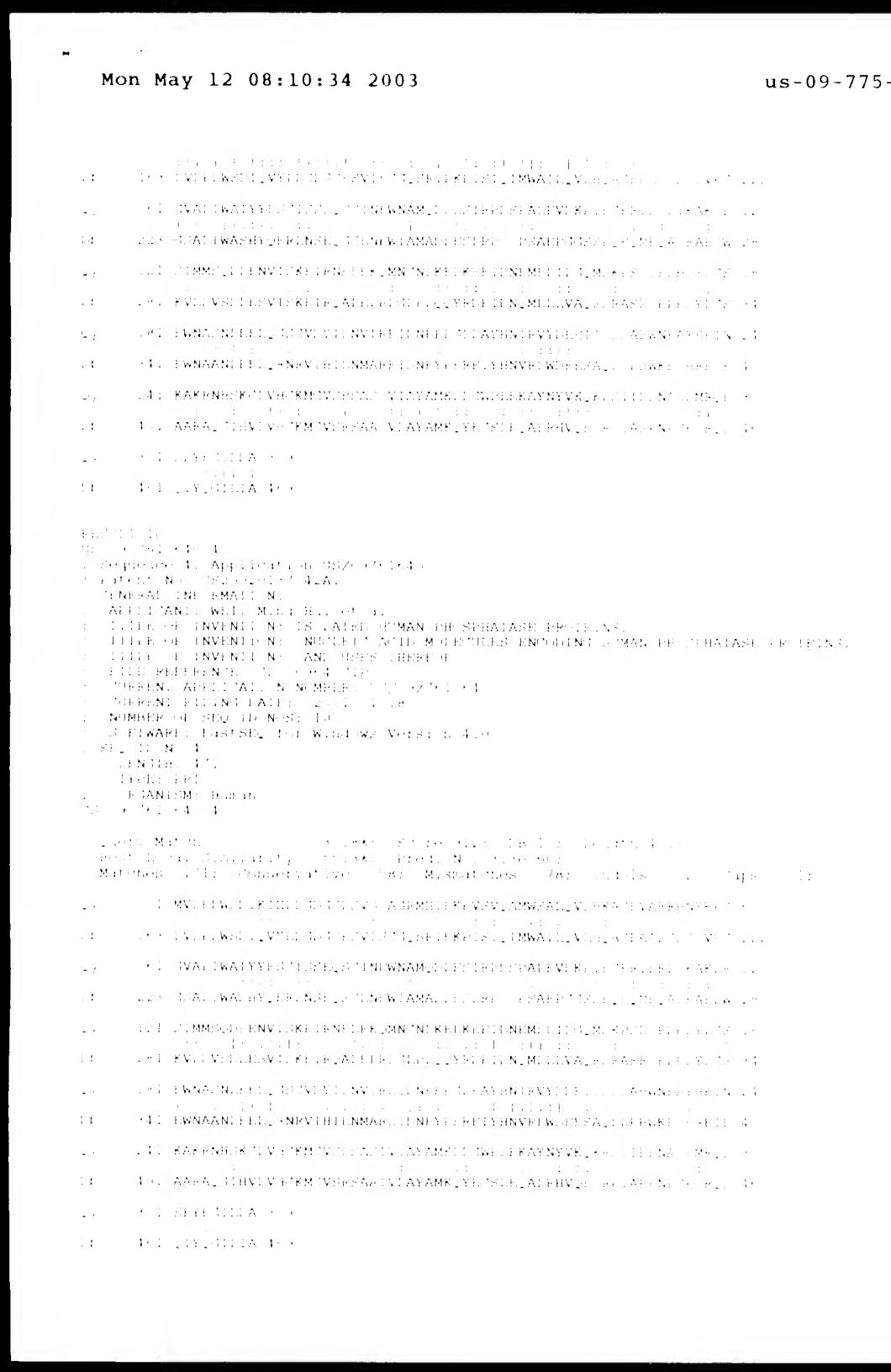

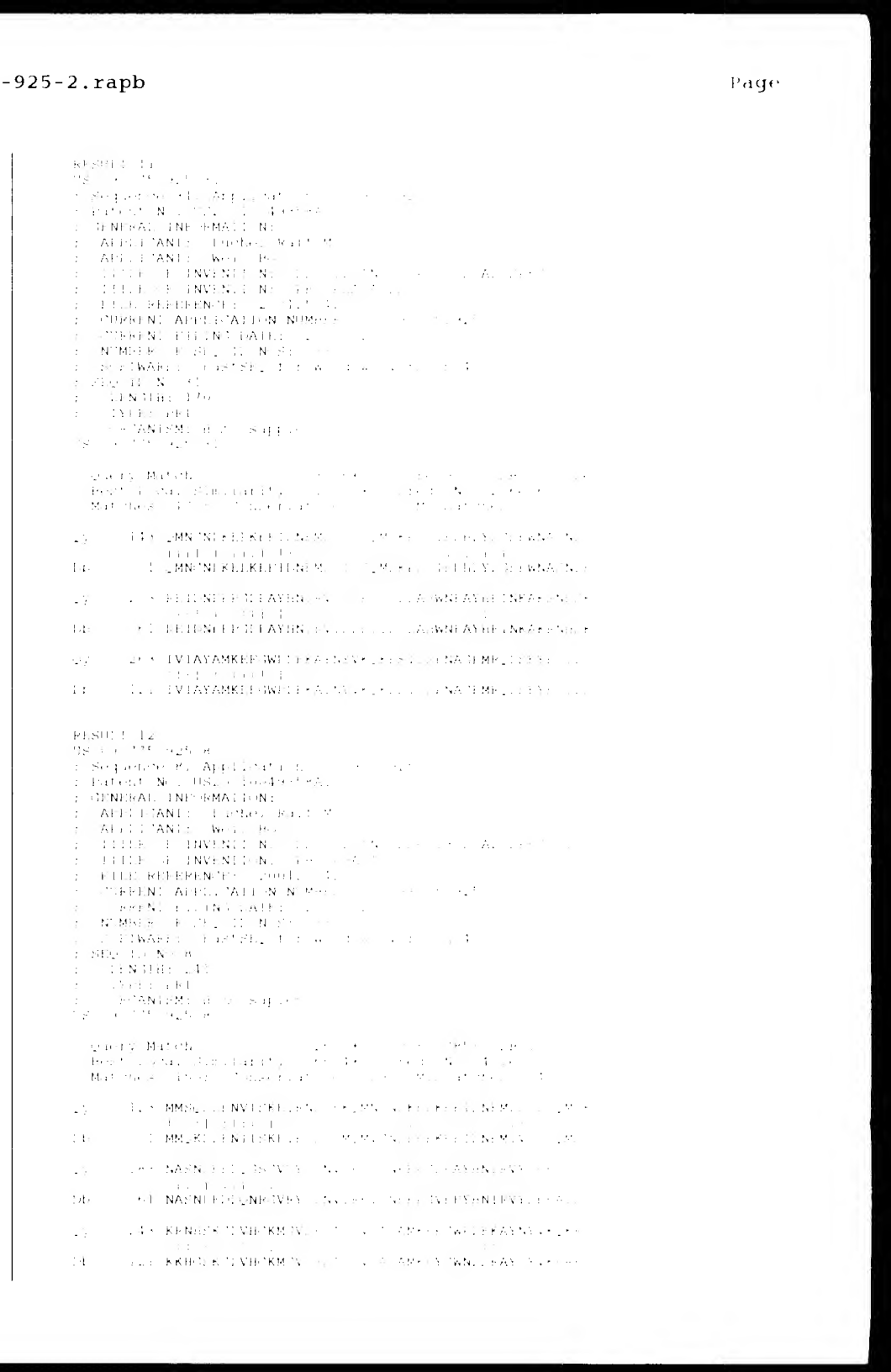

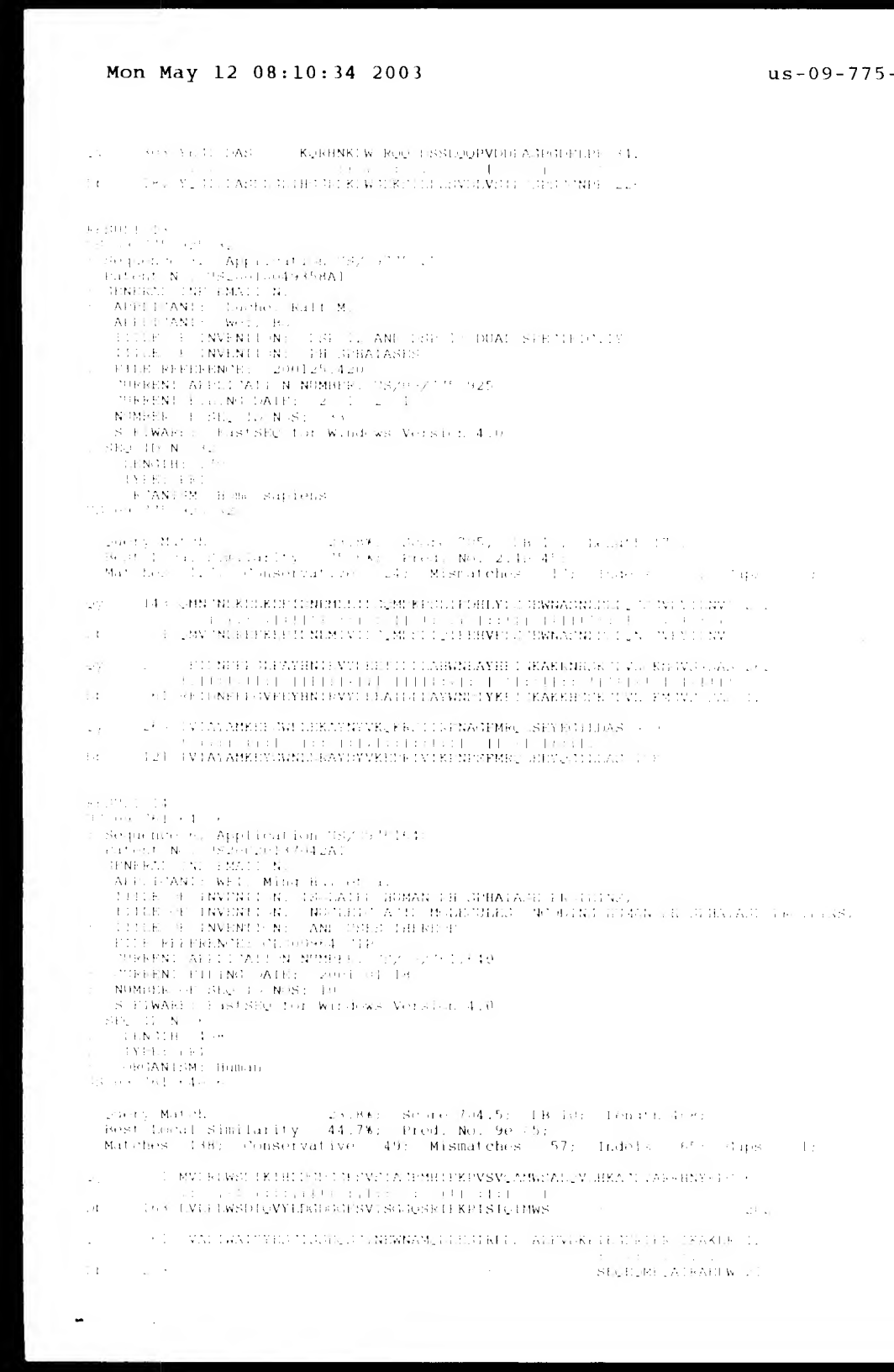

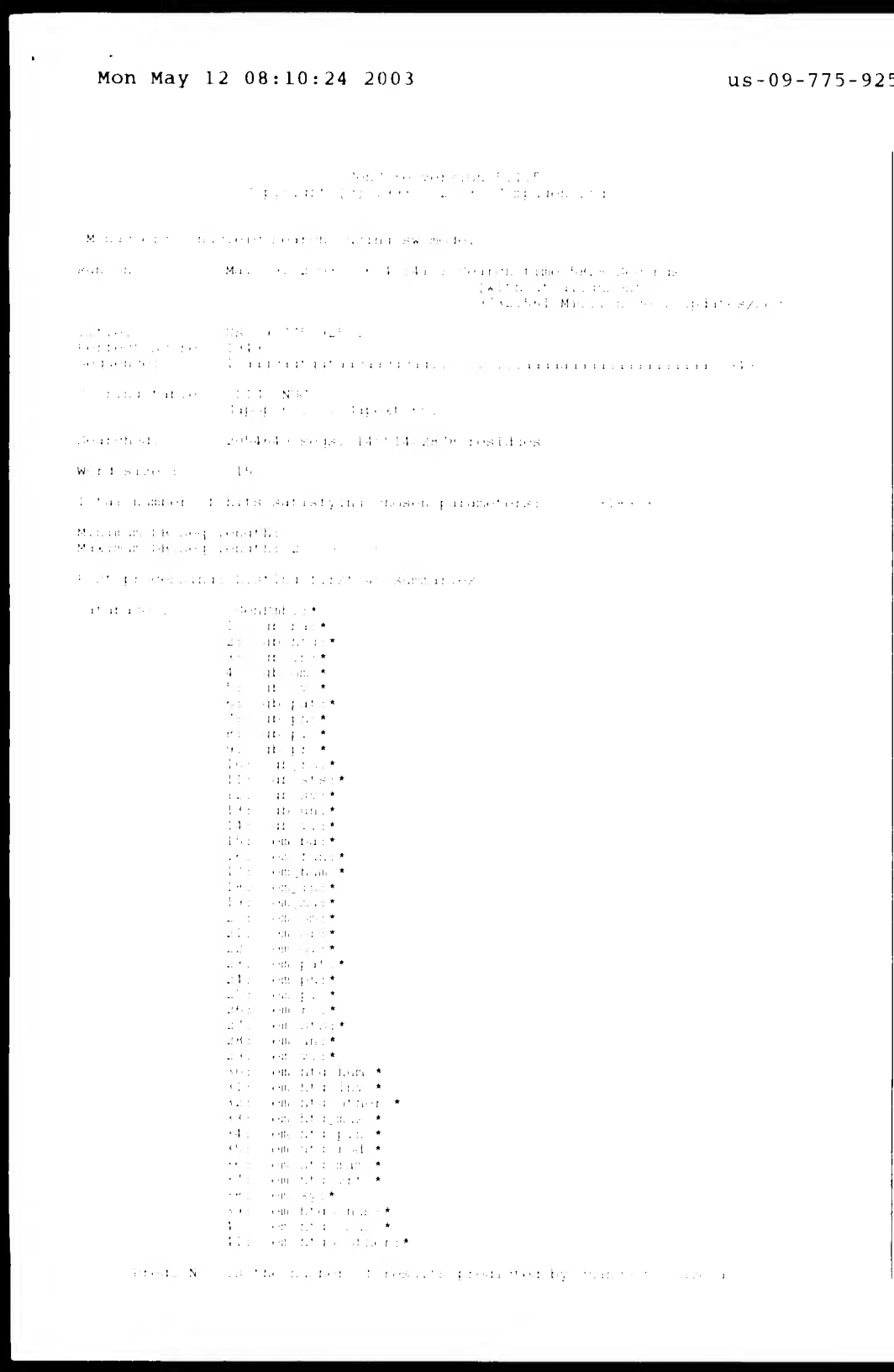

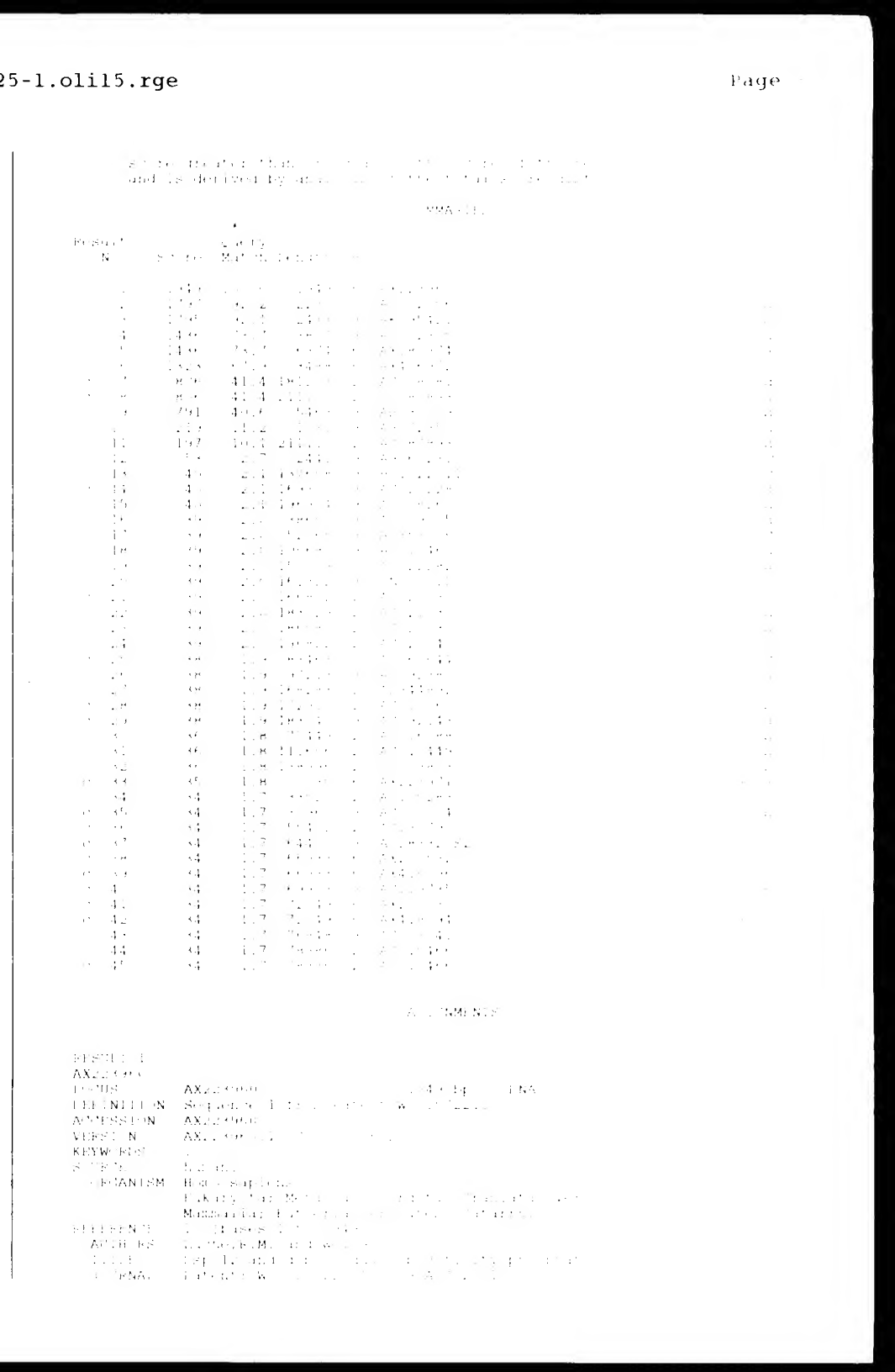

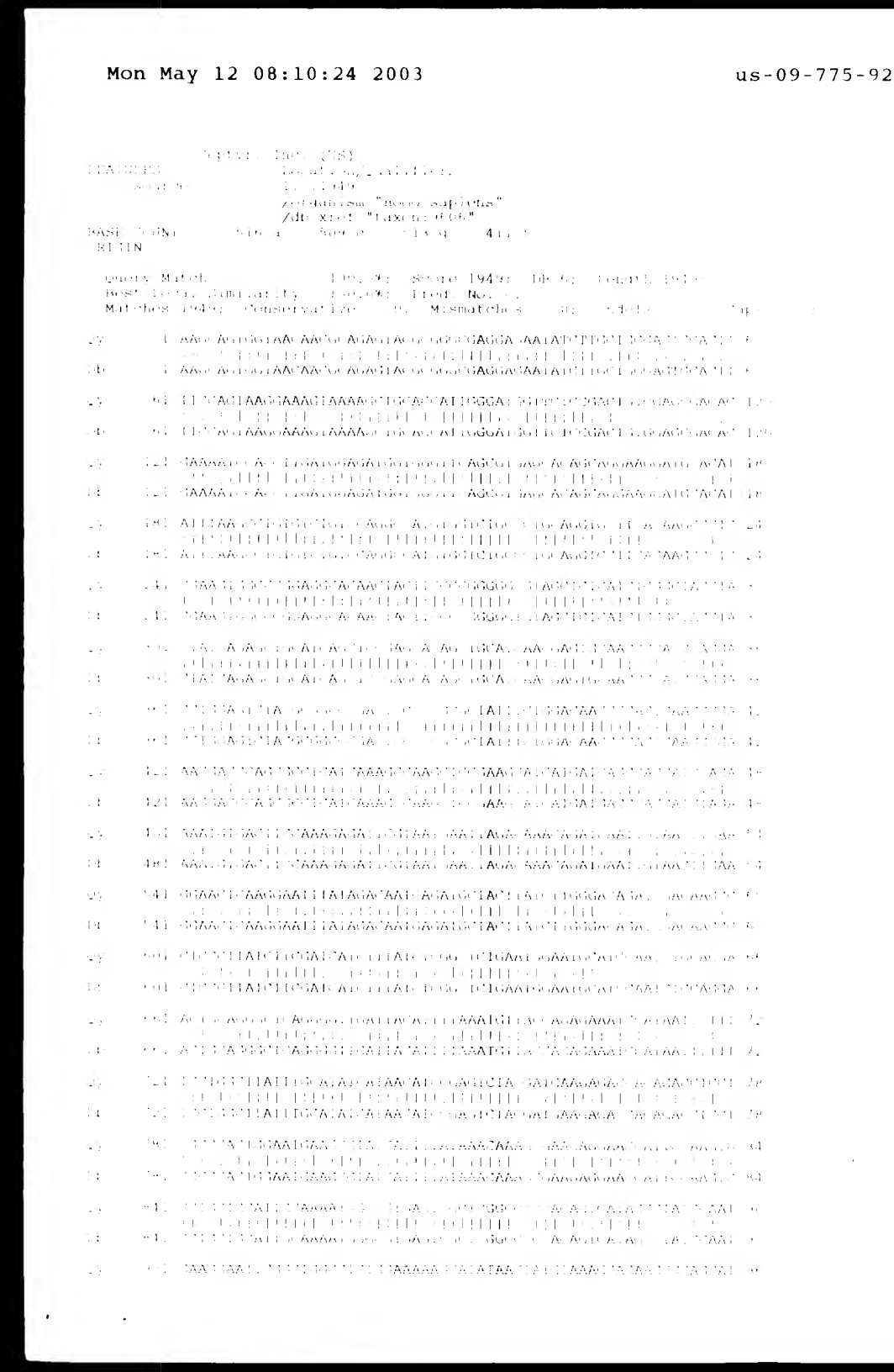

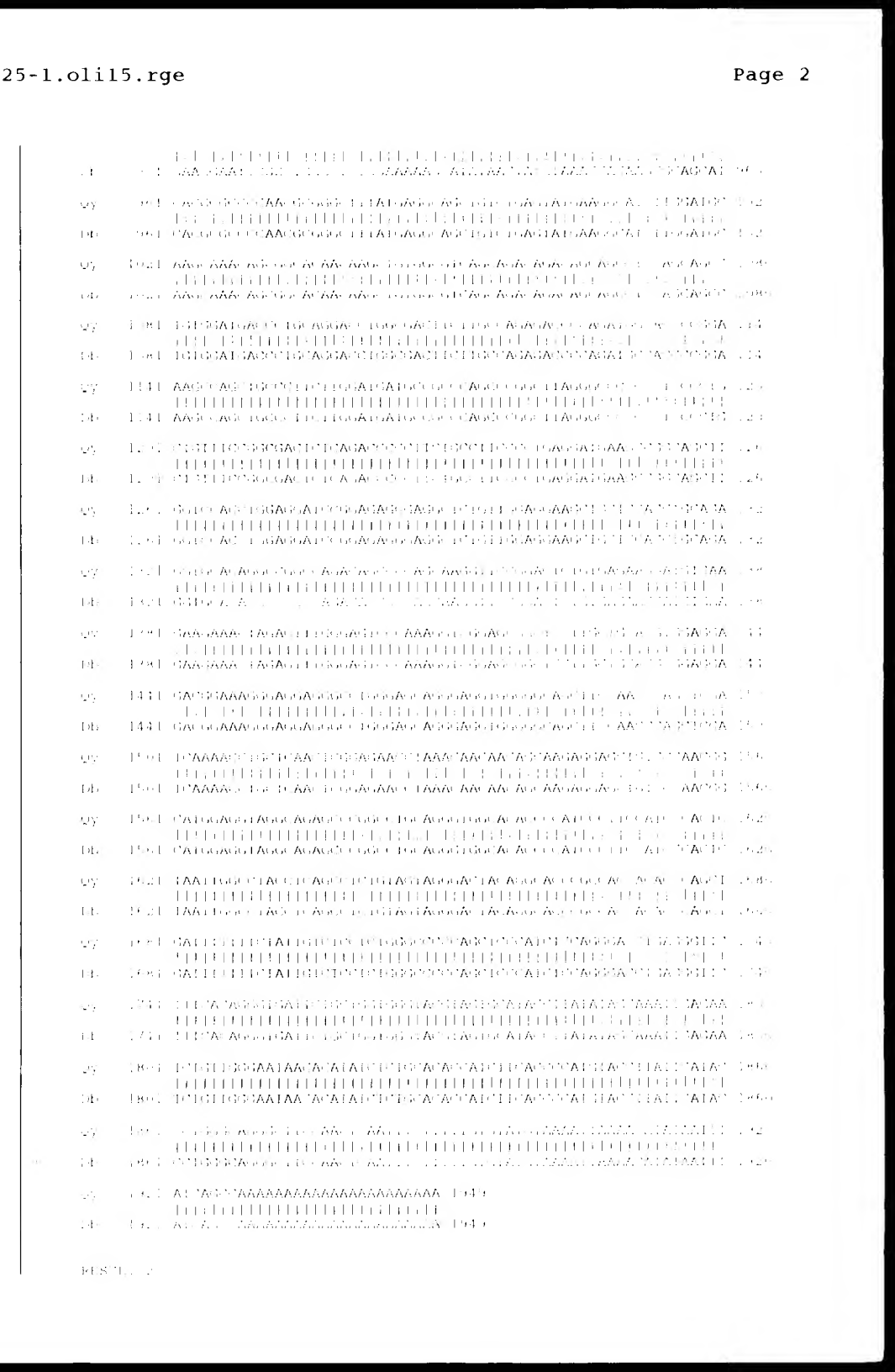

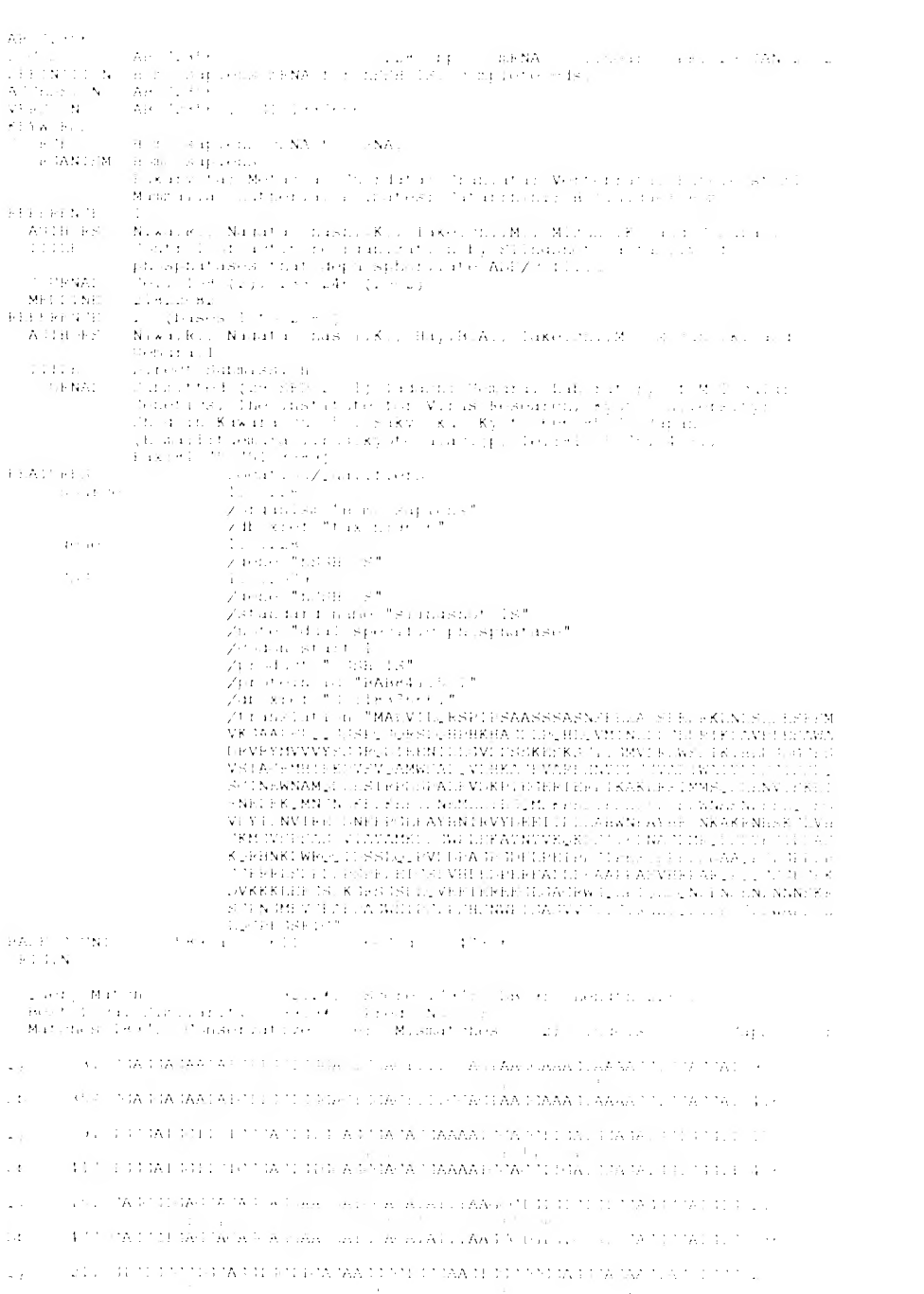

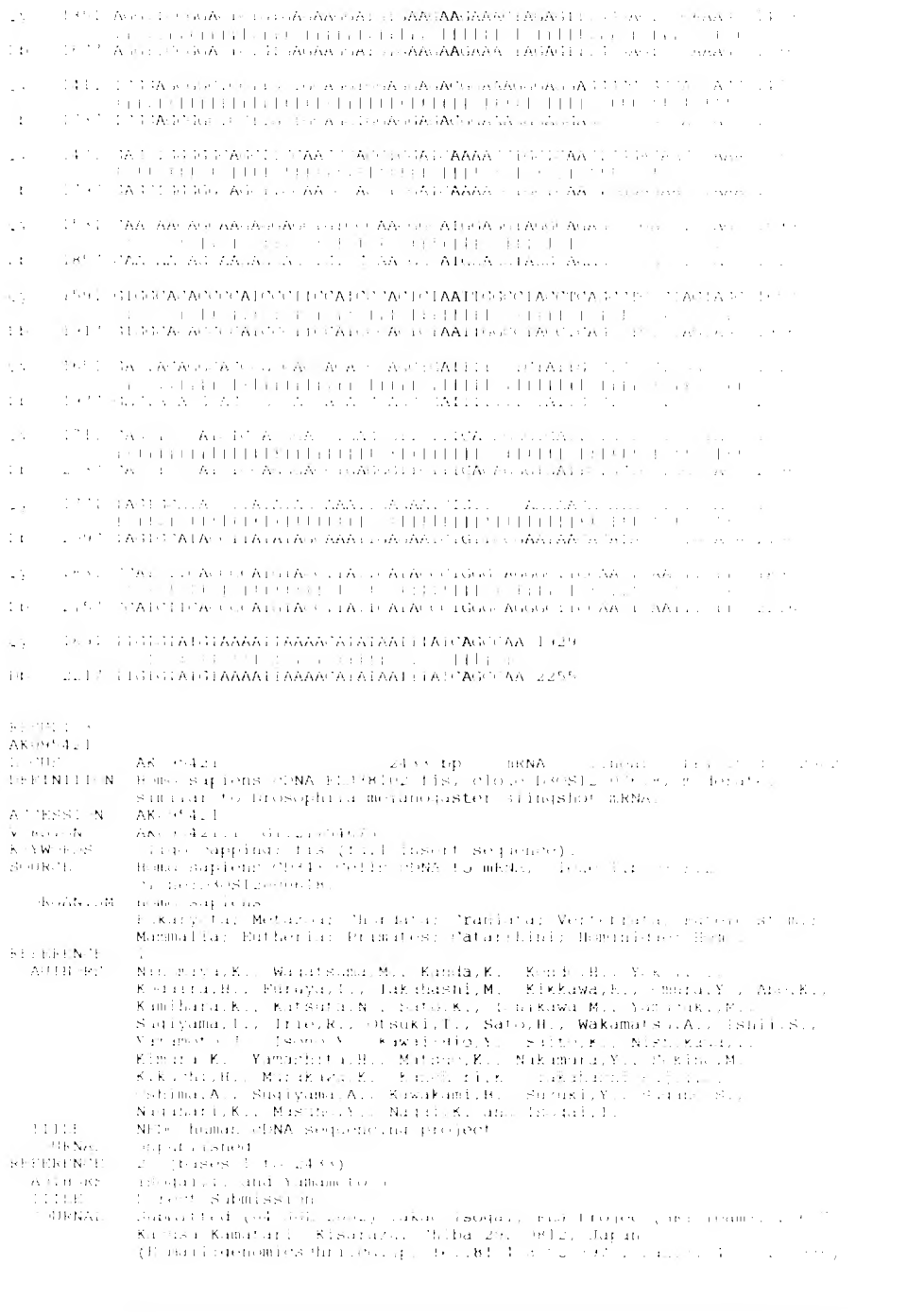

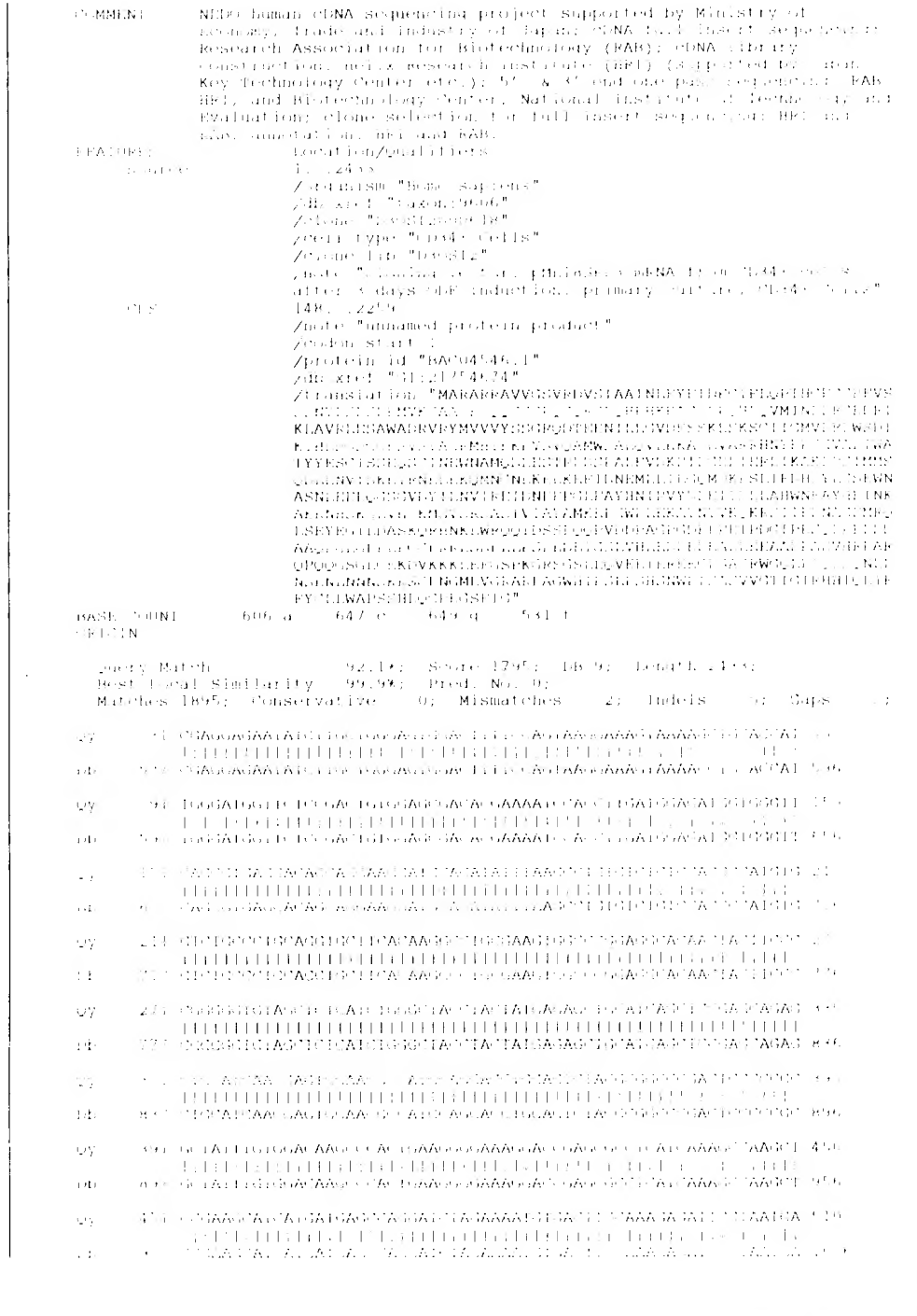

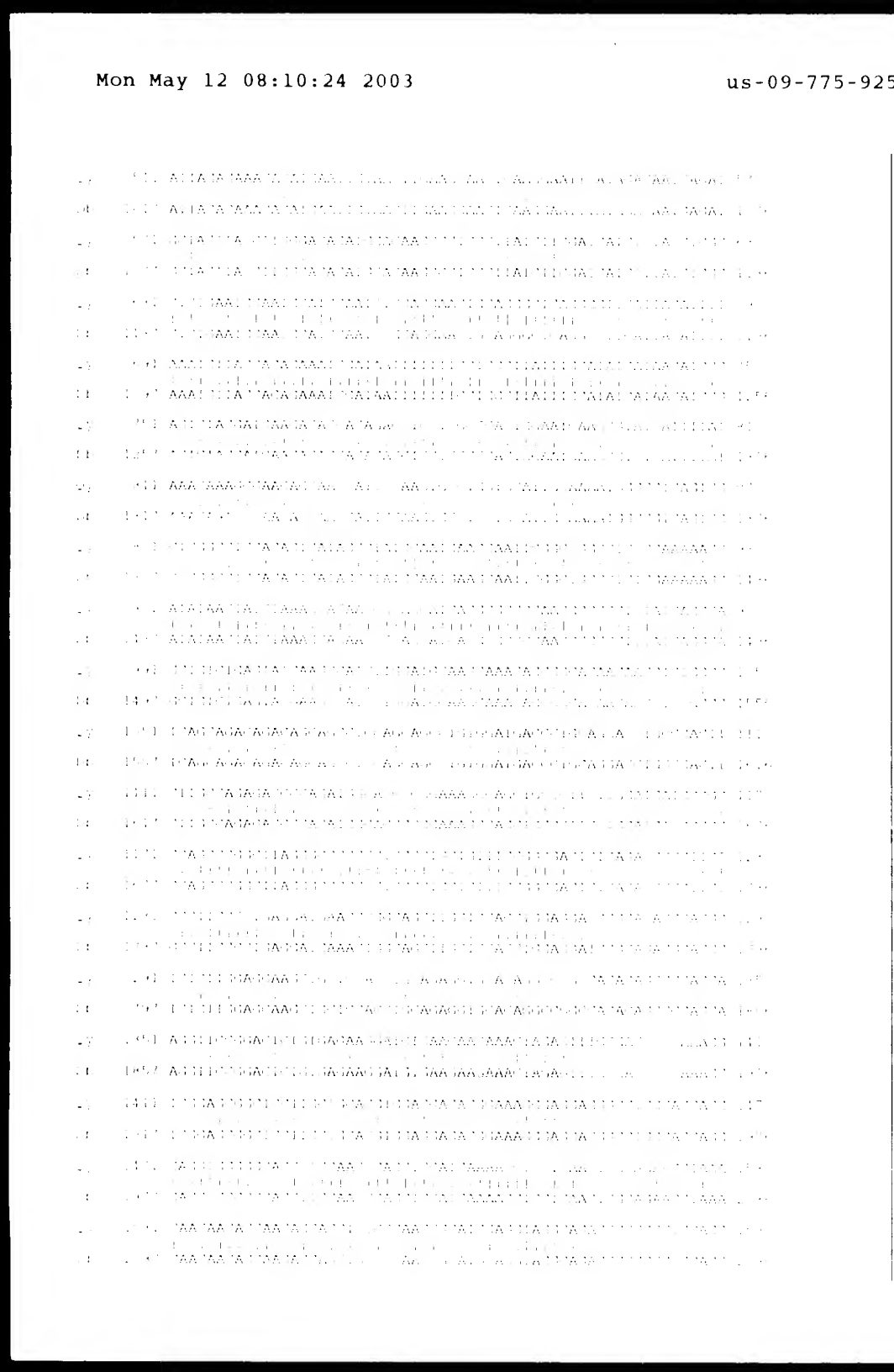

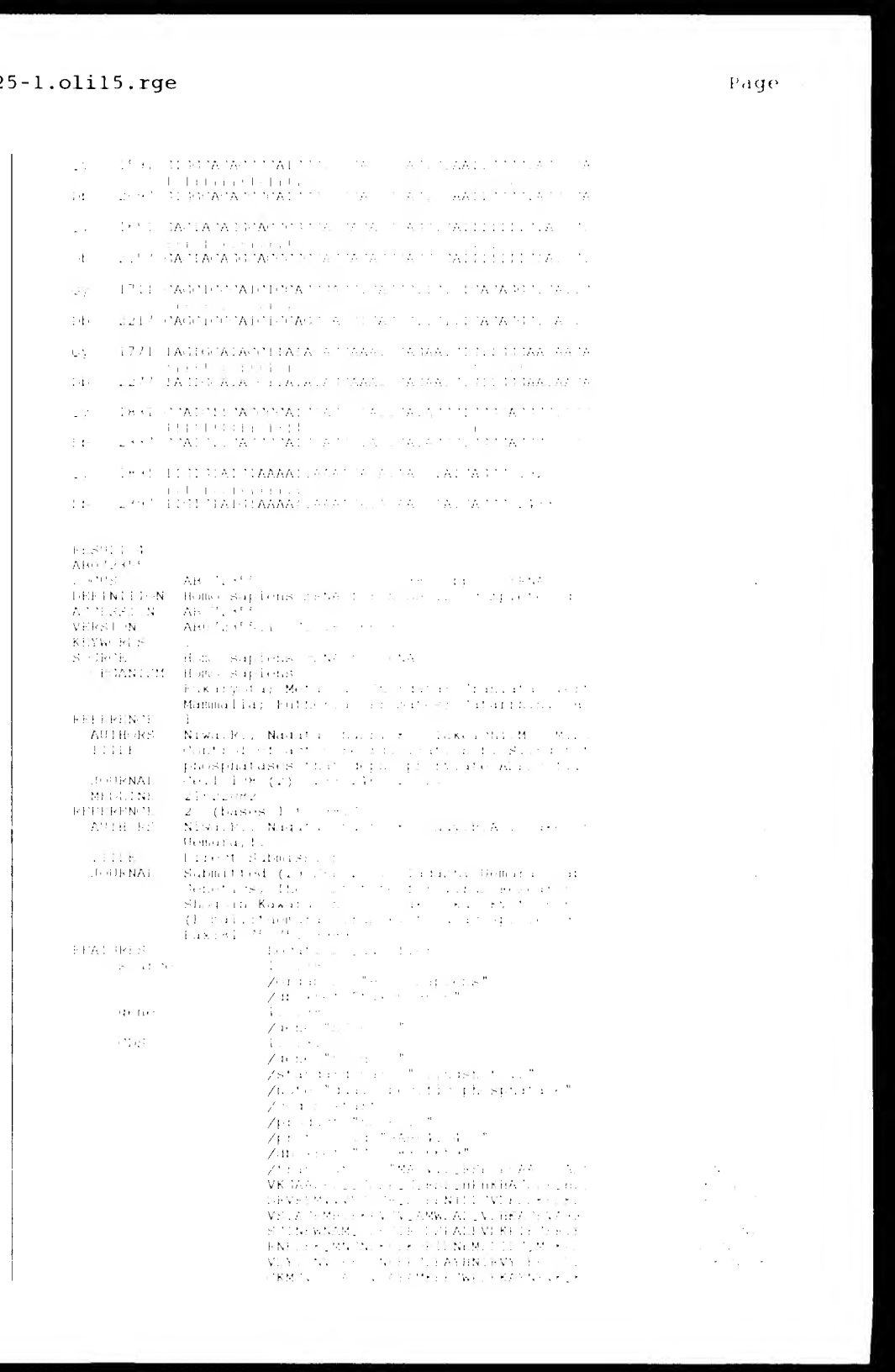

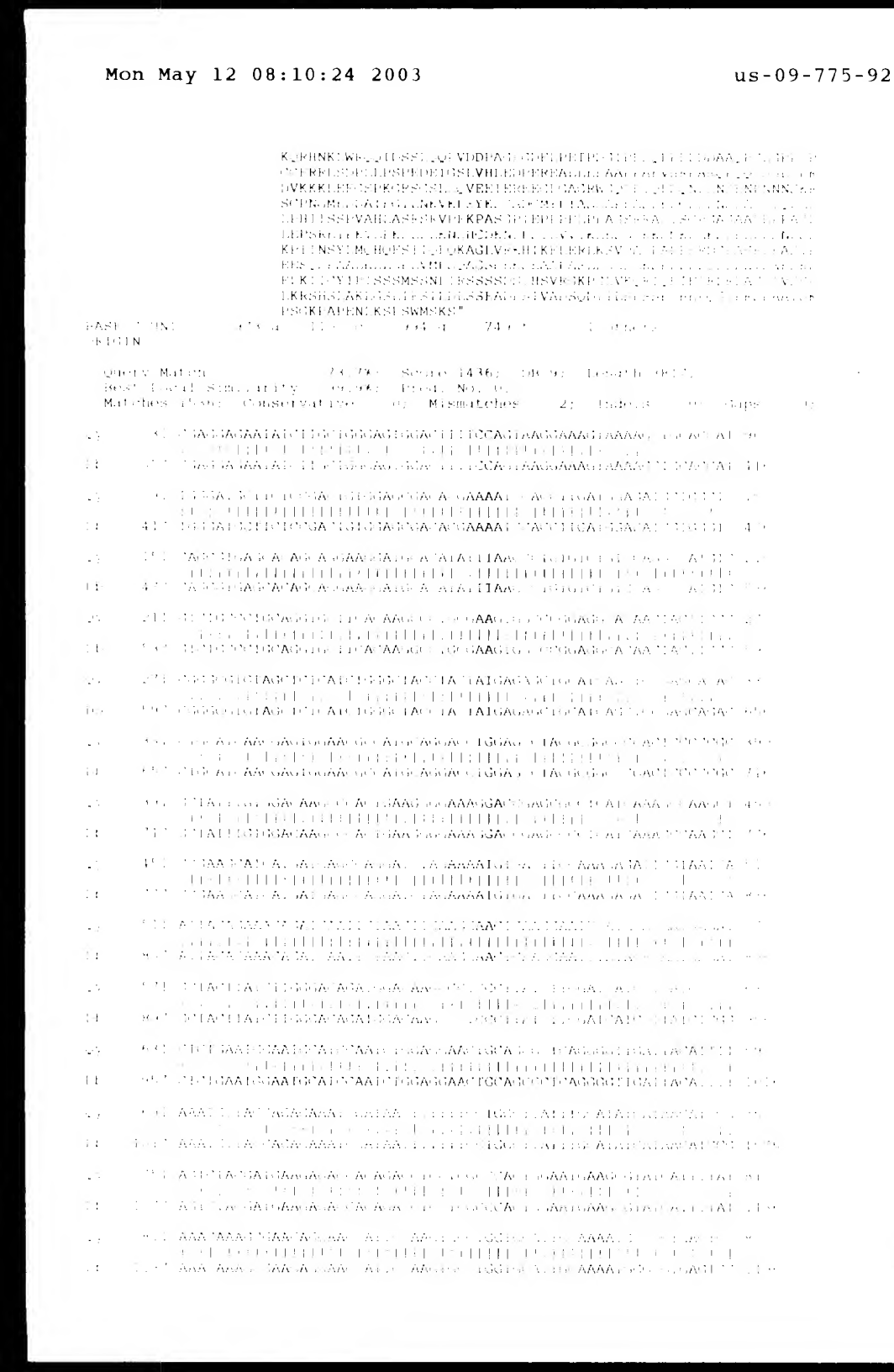

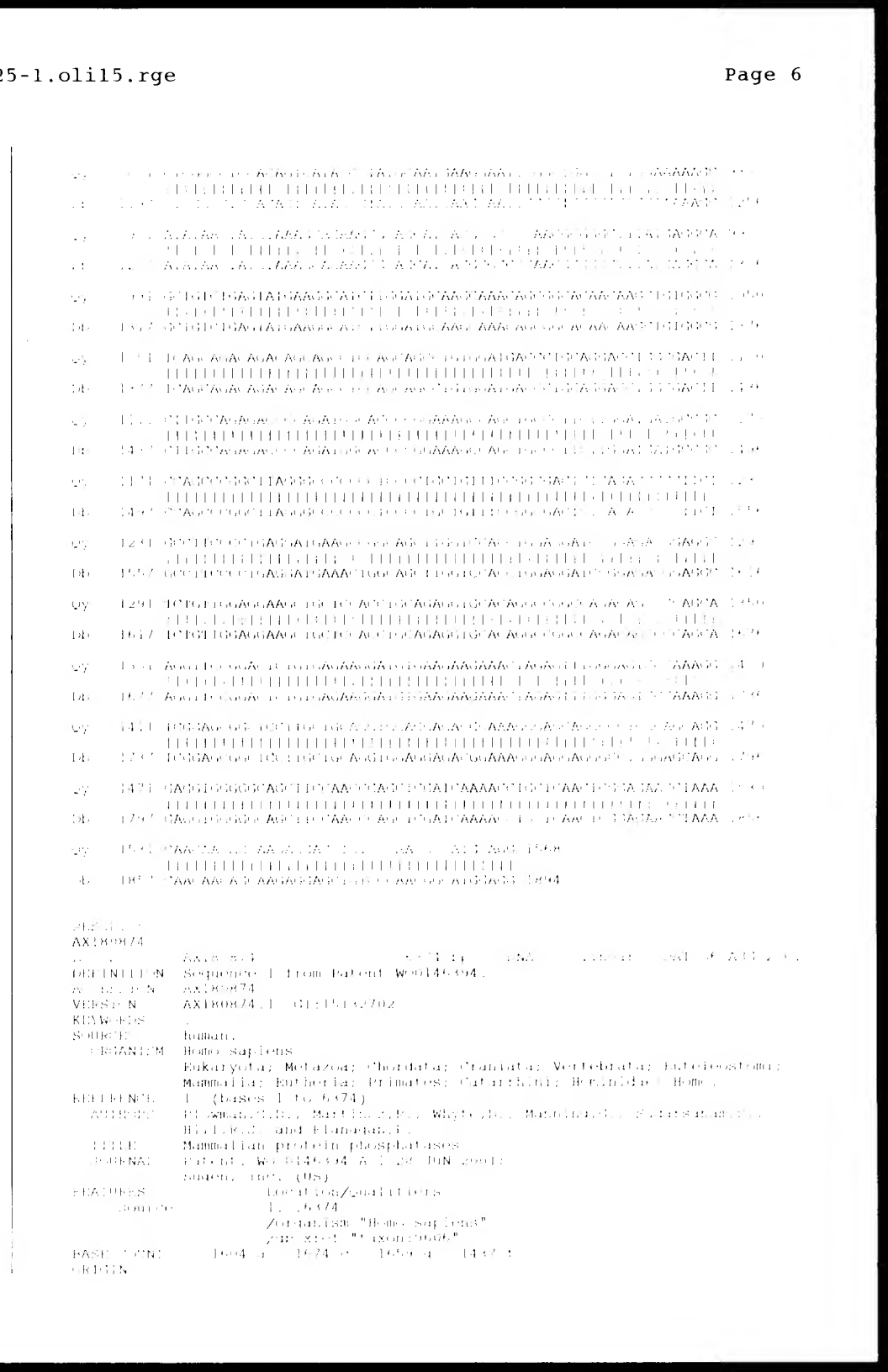

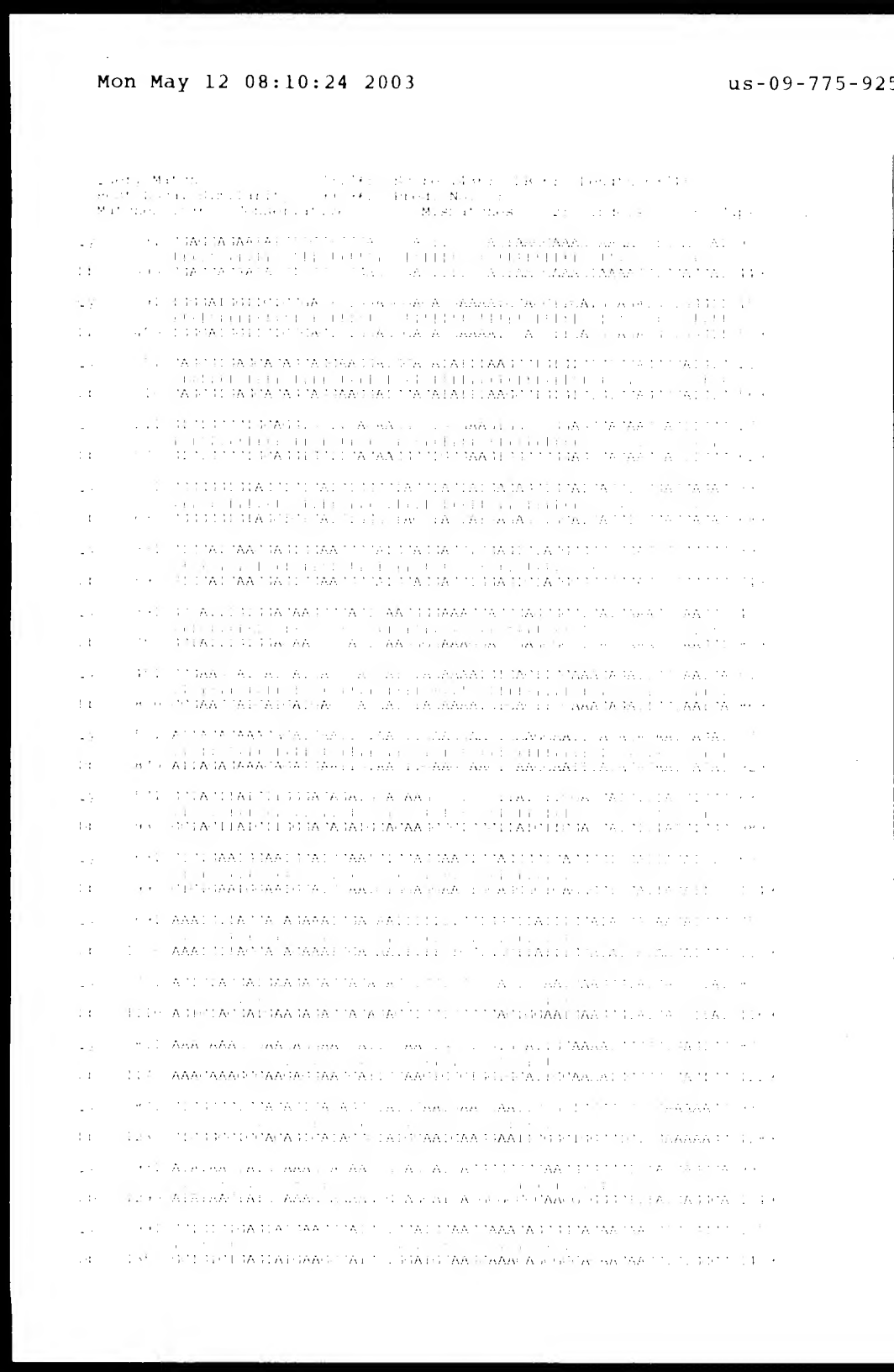

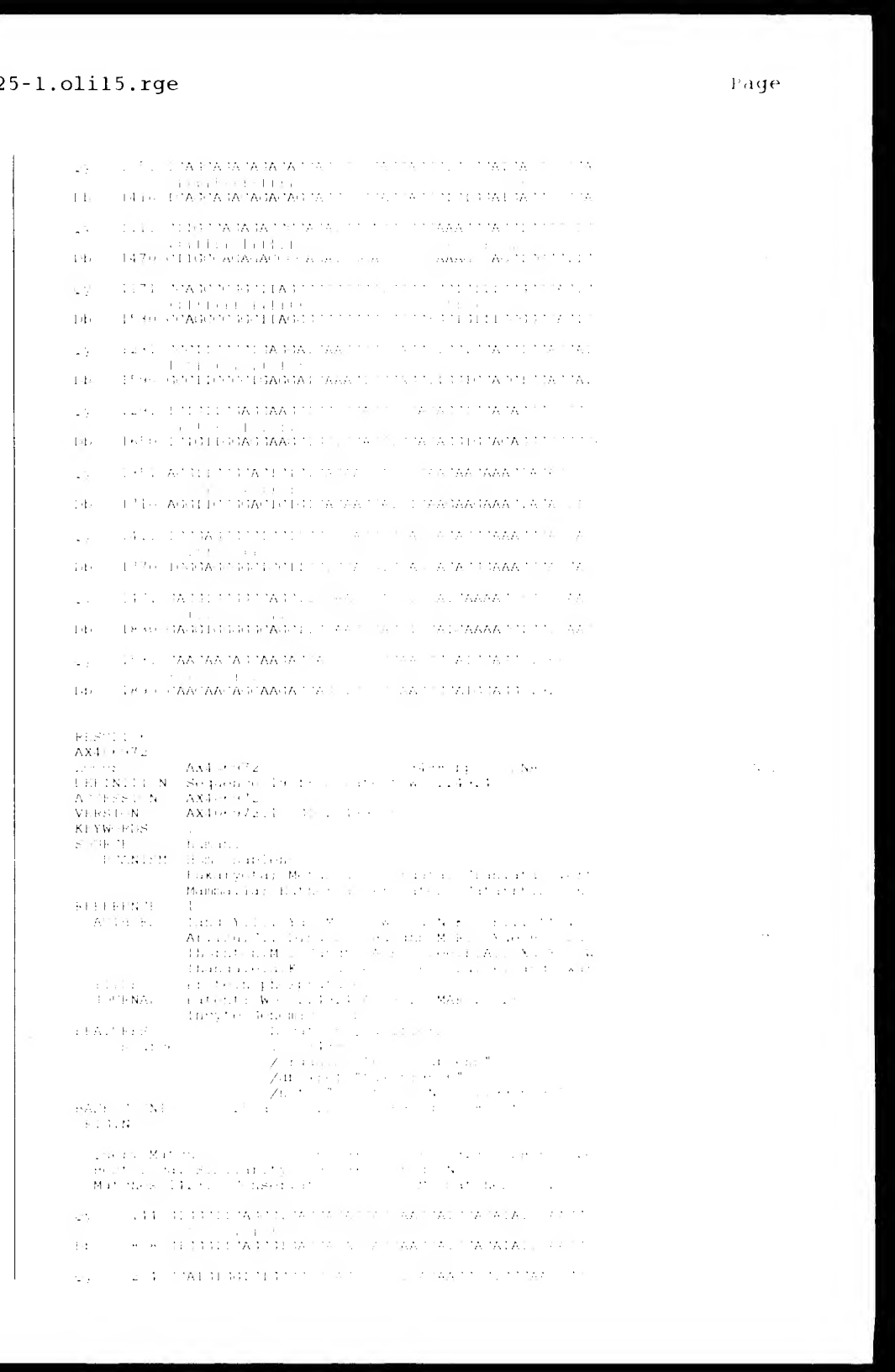

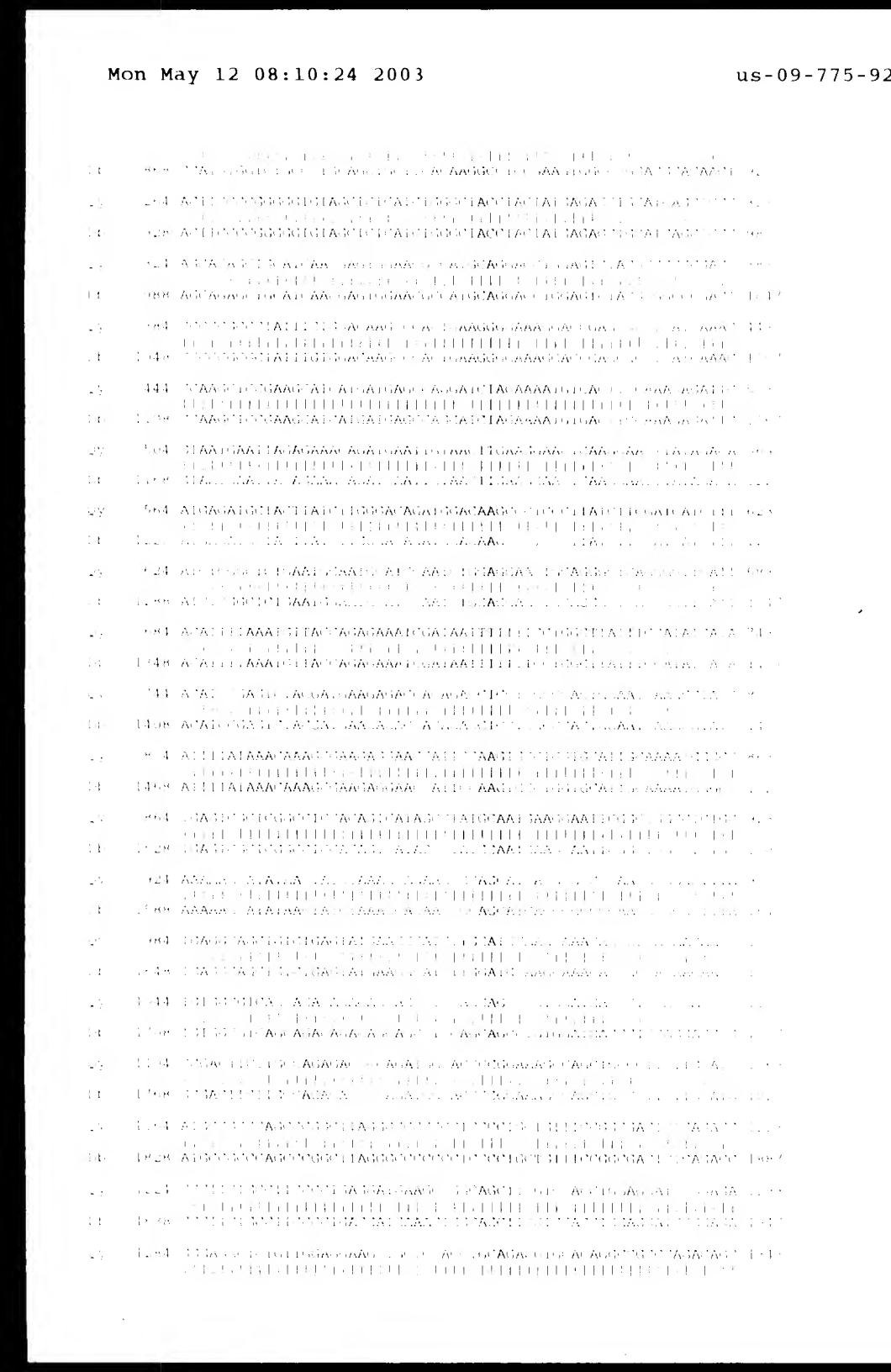

RESULT 2
AC000081/c
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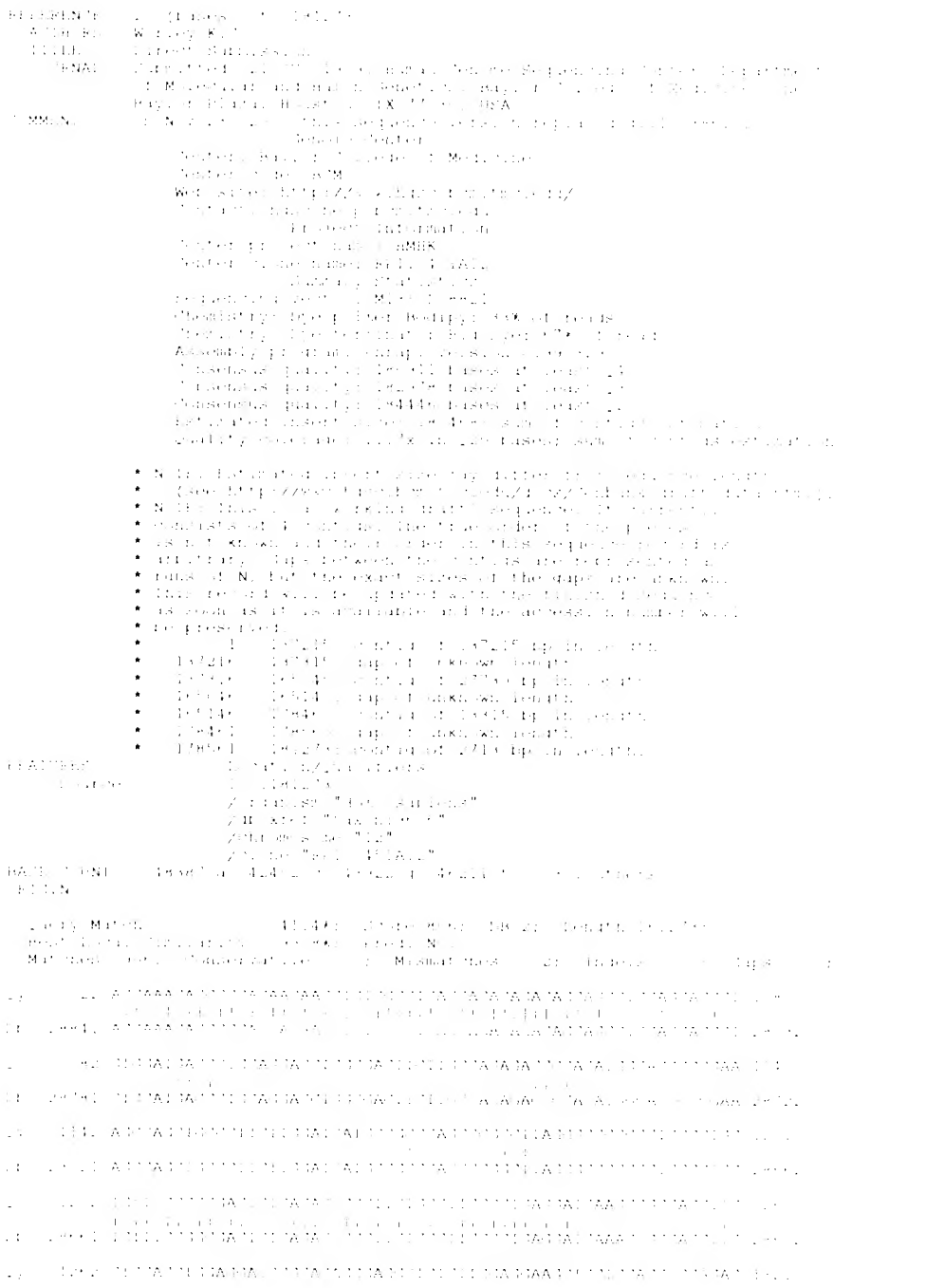
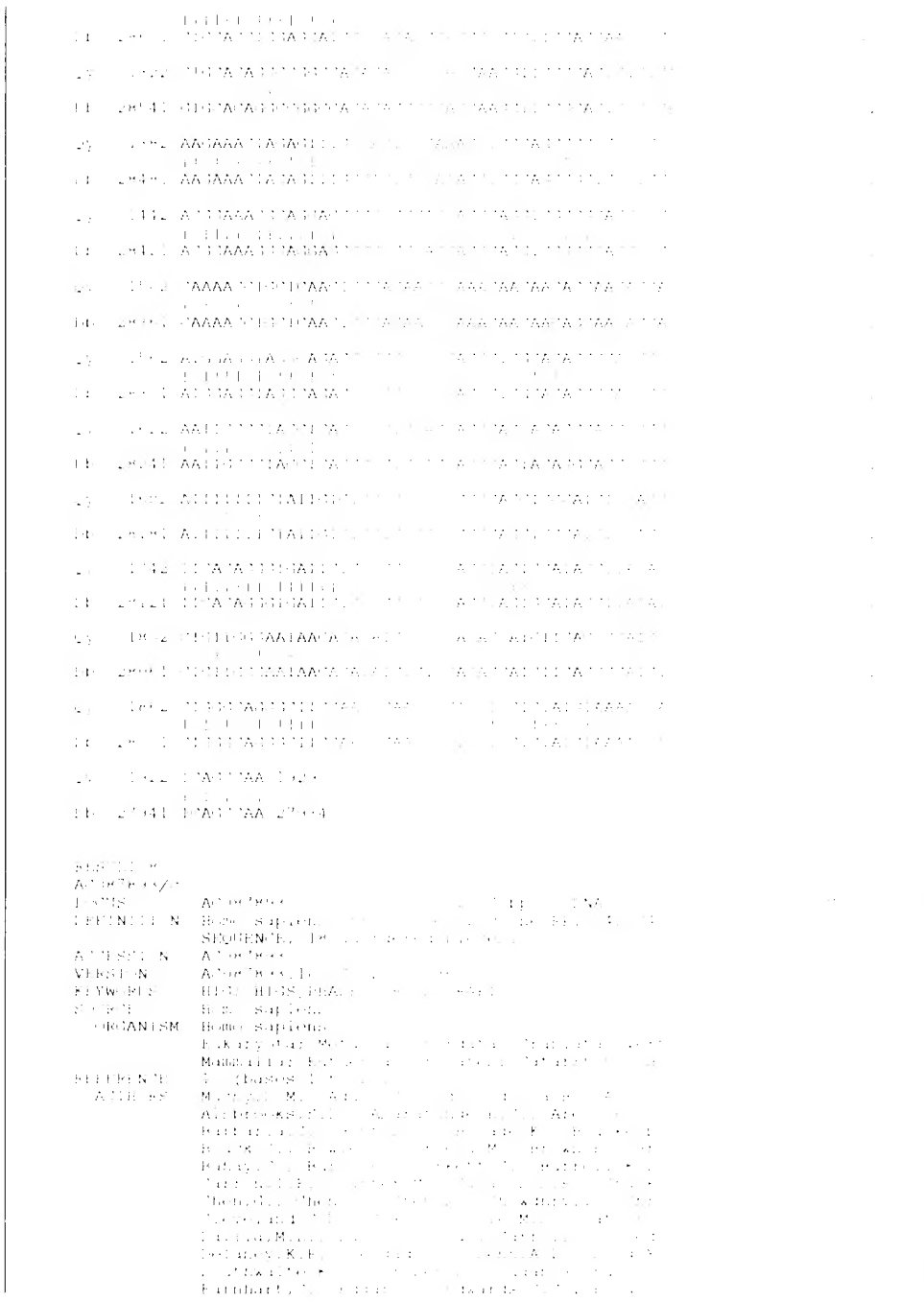
ACCESSION AC000081
VERSION AC000081.14 GI:11422790
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 181273)
AUTHORS M.Zody,E.M., Adams,C., Adio-Ebanks,R., Alexander,J.R., Alexandersson,K., Allen,S., Allgood,S., Amaratunga,N.C., Ambrose,K.D., Anderson,S., Barbazuk,J., Benton,D., Bimage,K., Blankenburg,K., Bonnin,D., Bonvicini,B., Borowsky,C., Bridgeman,M., Brown,S., Bryant,N., Burrill,W., Burton,J., Burrett,C., Carrell,L., Carter,M., Carvalho,C., Chen,H., Chen,K., Chen,Z., Chowdhary,I., Christopoulos,C., Cleveland,M., Cox,A., Coyle,M.B., Dahlke,S.R., David,R., Davis,M., Davis,C., Davy Carroll,L., Dederich,D.A., Delaney,K.K., Delehaunty,K., Dena,A.L., Dinh,H.H., Douglas-Wallwaite,K., Draper,B., Duquan-Rocha,S., Durbin,K.J., Earthrowl,M., Edgar,R., Edwards,J., Elhaj,O., Escoto,M., Faris,L., Ferraguto,D., Fiers,M., Ford,L., Foster,P., Frantz,P., Gabrisi,A., Gao,J., Garcia,A., Garner,L., Garza,K., Gaskell,K., Gatto,L.A., Gonzalez,W., Gonzalez,P., Greco,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Harland,J., Hawes,A., Hernandez,J., Hinzmann,B., Holden,M., Holland,R., Holloway,E., Honrubia,M., Hood,L., Hopkins,B., Howell,E., Howard,S., Huber,J., Hulyk,S., Humphray,S., Hunsicker,P., Hunt,A., Johnson,E., Johnson,D., Kamat,A., Kanga,S., Karlsson,E., Kelly,S., Khan,Z., Kimball,E., Kokkinaki,M., Kolar,R., Kolb,S., Kucaba,T., Kucherlapati,R., Kulikova,T., Kulp,D., Lacante,N., Lamb,J., Lamerdin,J., Landrum,M., Langford,C., Lee,J., Lehoczky,J., Levine,J., Lewis,L., Li,J., Li,Z., Liebhaber,S., Liu,C., Liu,X., Liu,W., Lloyd,C., Lovering,R., Lu,J., Lu,Y., Lucas,S., Lyne,R., Ma,J., Mahadevaiah,M., Majoros,W., Maloney,B., Mandrekar,A., Manning,J., Mardis,E., Marra,M., Martin,D., Martindale,A., Mashreghi-Mohammadi,M., Matthews,L., Mayer,K., Mazrieva,S., McCann,O., McClay,J., McDonald,S., McGuire,M., Mecklenburg,K., Meidanis,J., Menzies,A., Merante,F., Meyer,R., Millar,D., Mohabbat,K., Morgan,M., Morris,S., Moschonas,N., Mott,R., Mullikin,J., Muzny,D., Nandkeshwar,R., Narayan,K., Narayanan,V., Nefedov,M., Nelson,J., Newman,V., Newsham,I., Newsham,N., Nguyen,A., Nguyen,N., Nicol,R., Nikolaidis,N., Nobile,C., Nwankwo,S., Ogden,M., Okwuonu,G., Onyiah,C., Osoegawa,K., Ostrander,E., Ouellette,B., Parker,A., Patel,S., Patterson,J., Peacock,S., Pearman,C., Perez,J., Peters,I., Pickens,K., Primas,R., Pucci,J., Quiles,M., Rachupka,A., Raj,B., Rand,S., Rasolonjatovo,I., Reed,J., Rensing,L., Retta,S., Rhodes,S., Richardson,P., Richardson,D., Rodriguez,O., Rogers,J., Rogers,Y., Rose,C., Ross,M., Rotter,M., Roy,D., Ruiz,M., Russo,R., Sallee,J., Salzberg,S., Sanchez,A., Sanders,D., Sanders,R., Santos,R., Sapojnikov,V., Savery,G., Schein,J., Schein,H., Schmidt,R., Schuler,G., Scott,C., Screpanti,S., Segelsky,A., Shaw,S., Shen,H., Shi,M., Shneiderov,N., Shrivastava,S., Simmonds,P., Sisson,I., Sodergren,E., Sokolsky,I., Sparks,A., Steffen,D., Steinberg,K., Stone,H., Sutton,A., Swarbreck,A., Tabor,P., Tamberlan,A., Tamberlan,K., Tanaka,H., Tansey,J., Taylor,C., Taylor,J., Tolstoshev,C., Thomas,N., Thomas,S., Usmani,K., Vaquerizas,J., Vera,V., Villalobos,L., Vinson,J., Wall,R., Wang,S., Ward-Moore,S., Warren,K., Washington,C., Watkins,J., Weissenbach,J., Williams,G., Williamson,A., Wilmer,T., Wooden,S., Wortley,G., Wu,C., Wu,Z., Wu,T., Zhou,Y., Zody,M., Nelson,D., and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished





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Wilczek,E.; Wilhelm,R.; Williams,A.; Wilson,K.; Woodland,
Wu,J.; Wu,Y.; Wu,Y.F.; Zhou,J.; Zorrilla,S.; Nelson,J.
Weinstock,G. and Gibbs,R.

TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2111)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (08-FEB-2001) Human Genome Sequencing Center, Baylor College of Medicine, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 2111)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (09-MAY-2002) Human Genome Sequencing Center, Baylor College of Medicine, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Apr 28, 2002 this sequence version replaced gi:13111604.

Genome Center

Center: Baylor College of Medicine
Center code: BCM
WWW center URL: http://www.hgsc.bcm.tmc.edu
Contact: hgsc-help@hgsc.bcm.tmc.edu

Project Information

Center project name: BCMH
Center clone name: RP11-42A4
Summary Statistics
Sequencing vector: Plasmid
Chemistry: type terminator, BigDye 1.1
Assembly program: Phrap version 0.960423
Consensus quality: 2 or 3% bases at least Q9
Consensus quality: 204062 bases at least Q20
Consensus quality: 203798 bases at least Q30
Estimated insert size: 204516; amount bounds estimation
Quality coverage: 5x in 920 bases; sum of contig stretches = 1

* NOTE: Estimated insert size may differ from sequence length.
* (see http://www.hgsc.bcm.tmc.edu/projects/human/finishing.html)
* NOTE: This is a "working draft" sequence. It consists
* 1 of 5 sections. The true order of the pieces
* is not known, and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

*	1 - 1108	1108 bp; contig of 5968 bp in length
*	1109 - 1207	99 bp; gap of unknown length
*	1208 - 2297	1090 bp; contig of 5968 bp in length
*	2298 - 8265	5968 bp; contig of 5968 bp in length
*	8266 - 8365	100 bp; gap of unknown length
*	8366 - 13227	4862 bp; contig of 4862 bp in length
*	13228 - 13327	100 bp; gap of unknown length
*	13328 - 18391	5064 bp; contig of 5064 bp in length
*	18392 - 18491	100 bp; gap of unknown length
*	18492 - 26933	8442 bp; contig of 8442 bp in length
*	26934 - 26943	10 bp; gap of unknown length
*	26944 - 32810	5867 bp; contig of 6177 bp in length
*	32811 - 32910	100 bp; gap of unknown length
*	32911 - 39877	6967 bp; contig of 6967 bp in length
*	39878 - 39977	100 bp; gap of unknown length
*	39978 - 47399	7422 bp; contig of 7422 bp in length
*	47400 - 47499	100 bp; gap of unknown length
*	47500 - 54837	7338 bp; contig of 7338 bp in length
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*	54938 - 64585	9648 bp; contig of 9648 bp in length
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*	64686 - 73903	9218 bp; contig of 9218 bp in length
*	73904 - 74004	101 bp; gap of unknown length
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*	83712 - 83910	199 bp; gap of unknown length
*	83911 - 98697	14787 bp; contig of 14787 bp in length
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*	98898 - 111284	12387 bp; contig of 12387 bp in length
*	111285 - 111394	110 bp; gap of unknown length
*	111395 - 121062	9668 bp; contig of 9668 bp in length
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*	122063 - 142013	19951 bp; contig of 19951 bp in length
*	142014 - 142113	100 bp; gap of unknown length
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FEATURES	Location/Qualifiers	
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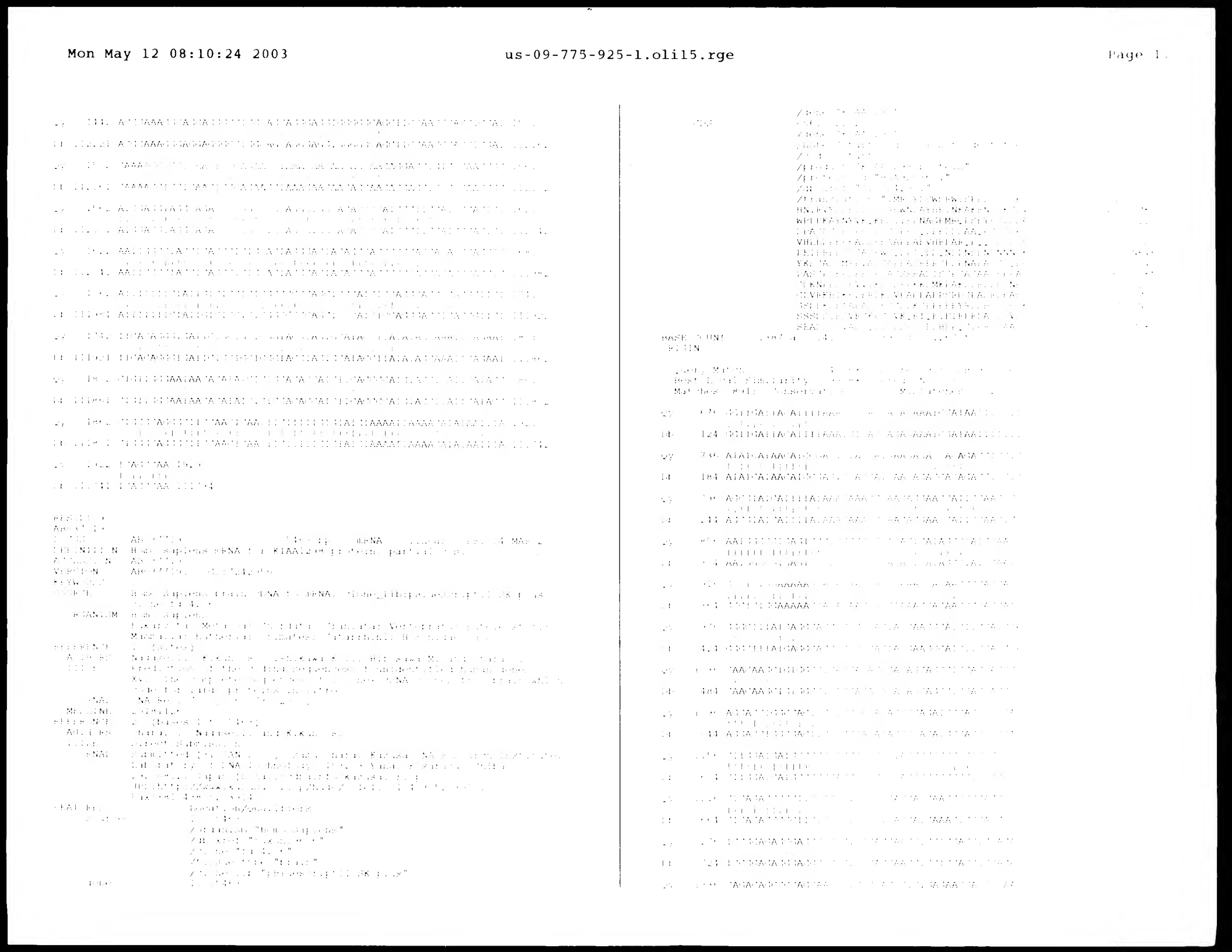
ORIGIN		



[illegible]

RESULT [illegible]
AB072357
LOCUS AB072357 [illegible] bp mRNA linear [illegible]
DEFINITION Homo sapiens mRNA for hSSH-1B, complete cds.
ACCESSION AB072357
VERSION AB072357.1 GI:18376662
KEYWORDS .
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE [illegible]
AUTHORS Niwa,R., Nagata-Ohashi,K., Takeichi,M., Mizuno,K. and Uemura,T.
TITLE Control of actin reorganization by Slingshot, a family of phosphatases that dephosphorylate ADF/cofilin.
JOURNAL Cell 108 (2), [illegible] (2002)
MEDLINE [illegible]
REFERENCE 2 (bases 1 to [illegible])
AUTHORS Niwa,R., Nagata-Ohashi,K., Hay,B.A., Takeichi,M., Mizuno,K. and Uemura,T.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-2001) Tadashi Uemura, Laboratory of Molecular Genetics, The Institute for Virus Research, Kyoto University; Shogoin Kawahara-cho 53, Sakyo-ku, Kyoto 606-8507, Japan (E-mail:tuemura@virus.kyoto-u.ac.jp, Tel:81-75-751-[illegible], Fax:81-75-751-4089)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 11.2%; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity 100.0%; Pred. No. 8.[illegible]e-111;
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[illegible]

RESULT [illegible]
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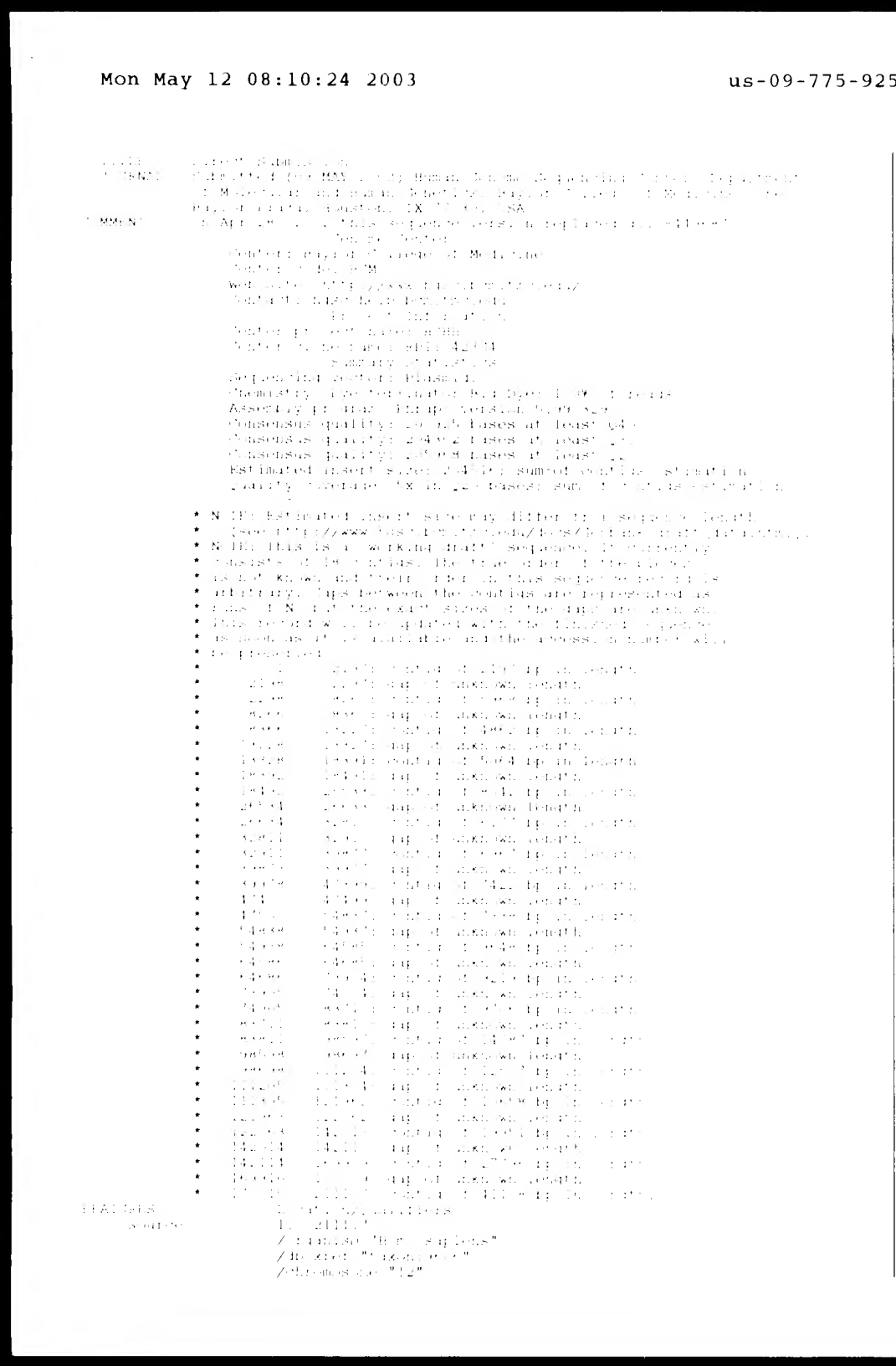
LOCUS AC087893 211117 bp DNA linear HTG [illegible]-MAY-2002
DEFINITION Homo sapiens chromosome 12 clone RP11-[illegible], WORKING DRAFT SEQUENCE, 18 unordered pieces.
ACCESSION AC087893
VERSION AC087893.18 GI:2033[illegible]
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 211117)
AUTHORS Muzny,D.M., Adams,[illegible], Adio-Oduola,B., Ali-Osman,F.[illegible], Allen,[illegible], Alsbrooks,S.L., Amaratunge,[illegible], Ate,[illegible], Ayele,M., Banks,[illegible], Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,[illegible], Bouck,[illegible], Bowie,S., Brizuela,M., Brown,E., Brown,M., Bryant,N.[illegible], Buhay,C., Burch,P., Burkett,C., Burrell,K.[illegible], Byrd,N.[illegible], Carron,[illegible], Carter,M., Cavazos,S.R., Chacko,[illegible], Chavez,[illegible], Chen,G., Chen,R., Chen,Z., Chowdhury,[illegible], Christopoulos,[illegible], Cleveland,C.D., Cox,[illegible], Coyle,M.[illegible], [illegible], Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,[illegible], Delaney,K.R., Delgado,[illegible], Denn,A.[illegible], [illegible], Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,[illegible], [illegible], Edwards,[illegible], [illegible], Falls,[illegible], Ferraguto,D., Flagg,N., Ford,J., Foster,[illegible], Frantz,P., Gabisi,A., Gao,[illegible], Garcia,A., Garner,[illegible], Garza,N., [illegible], Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,[illegible], Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,[illegible], Hollins,B., Hoseini,[illegible], Howard,S., Huber,[illegible], Hulyk,S., Hume,[illegible], Jackson,[illegible], Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., [illegible], Karlsson,[illegible], Kelly,S., Khan,[illegible], King,[illegible], Korvin,[illegible], Kovar,[illegible], Kratovic,J., Kureshi,A., Landry,N., [illegible], Lewis,L., Li,J., Li,Z., Lichtarge,[illegible], Liu,[illegible], Liu,[illegible], Li,W., Loulseged,H., Lozado,R.J., Lu,X., [illegible], [illegible], Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,[illegible], Massey,[illegible], Mawhiney,[illegible], McLeod,M.P., Meador,M., [illegible], Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,[illegible], Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,[illegible], Nwokenkwo,S., Ogah,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Perry,[illegible], Perez,[illegible], Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojalekan,[illegible], Ruiz,[illegible], Savery,[illegible], Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,[illegible], Sodergren,E., [illegible], Sparks,A., Stanley,[illegible], [illegible], Sutton,A., [illegible], Tabor,[illegible], Tamerisa,[illegible], [illegible], Tamez,H., Tansey,[illegible], Taylor,[illegible], Taylor,[illegible], Telford,B., Thomas,N., Thomas,[illegible], Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,[illegible], Wang,S., Ward-Moore,S., Warren,R., Washington,[illegible], Wellington,S., Williams,G., Williamson,A., Wleczyk,[illegible], Wooden,[illegible], Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,[illegible], Weinstock,G. and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 211117)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (0[illegible]-FEB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 211117)
AUTHORS Worley,K.C.



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  Matches    54;  Conservative    0;  Mismatches    0;  Indels    18;  Gaps    1;

Qy      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 60
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LOCUS       HS_2211                 19758 bp    DNA     linear   PRI 12-MAR-2003
DEFINITION  Human DNA sequence from clone RP5-922I1 on chromosome
            20q13.13-20q13.2 Contains a pseudogene similar to mouse
            interferon induced differentiation associated protein 3 gene
            ESTs, STSs and GSSs, complete sequence.
ACCESSION   AL049765
VERSION     AL049765.16  GI:5902588
KEYWORDS    IFI 3 differentiation associated protein.
SOURCE      human
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19758)
  AUTHORS   Lucas,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-2003) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
            Keywords: clonerequest"sanger.ac.uk"
COMMENT     On Sep 28, 1999 this sequence version replaced gi:5873483.
            Initial sequence assembly data is prepared from overlapping HTG3 phase
            0 entries. Where differences are found these are annotated as variations
            together with a note of the overlapping clone(s). Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            1-2 kb overlap as described above.
            The following abbreviations are used to describe primary accession
            numbers given in the feature table with their source database:
            EMBL: AC; GENBANK: ; REFSEQ: NT_; TPA: ; TPA_EXP: .
            The WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep
            This sequence was finished as follows: Gaps (Ns) in the finished
            sections were either double-stranded or sequenced with matching
            chemistry (e.g. read 1 with primer A, read 2 with primer B).
            An attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            two plasmid subclones or more than one M13 subclone and the
            assembly was confirmed by restriction digest. RP1-922I1 is a clone
            in the library RPCI-5, constructed by Ian Dunham and Eric Birney.
            Further details see
            http://www.sanger.ac.uk/HGP/Chr20.
            Visit EMBL-bank
            IMPORTANT: This sequence is not the entire insert in this
            BAC clone as it may be shorter because we sequence overlapping
            sections only once, except for a 1kb base overlap.
            The true left end of clone RP5-1022I1 is at 1 in this sequence.
            The true left end of clone RP4-724B5 is at 1956, in this sequence.
            The true right end of clone RP4-584C8 is at 1468 in this sequence.
FEATURES             Location/Qualifiers
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                     /clone_lib="RPCI-5"
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     repeat_region   60..105
                     /note="MER12B repeat; matches 58% of consensus"
     repeat_region   97..142
                     /note="25 copies of 2-mer at 92% conserved"
     repeat_region   106..141
                     /note="35 copies of 2-mer in 2-6% conserved"
     repeat_region   143..483
                     /note="Mir2c repeat; matches 59% of consensus"
     repeat_region   488..610
                     /note="L2 repeat; matches 24% of consensus"
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                     /note="match: SSS: EMBL:AQ220[3-4"
     repeat_region   778..1025
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     repeat_region   1472..1833
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     repeat_region   3191..3375
                     /note="MER66A repeat; matches 27% of consensus"
     repeat_region   3378..4519
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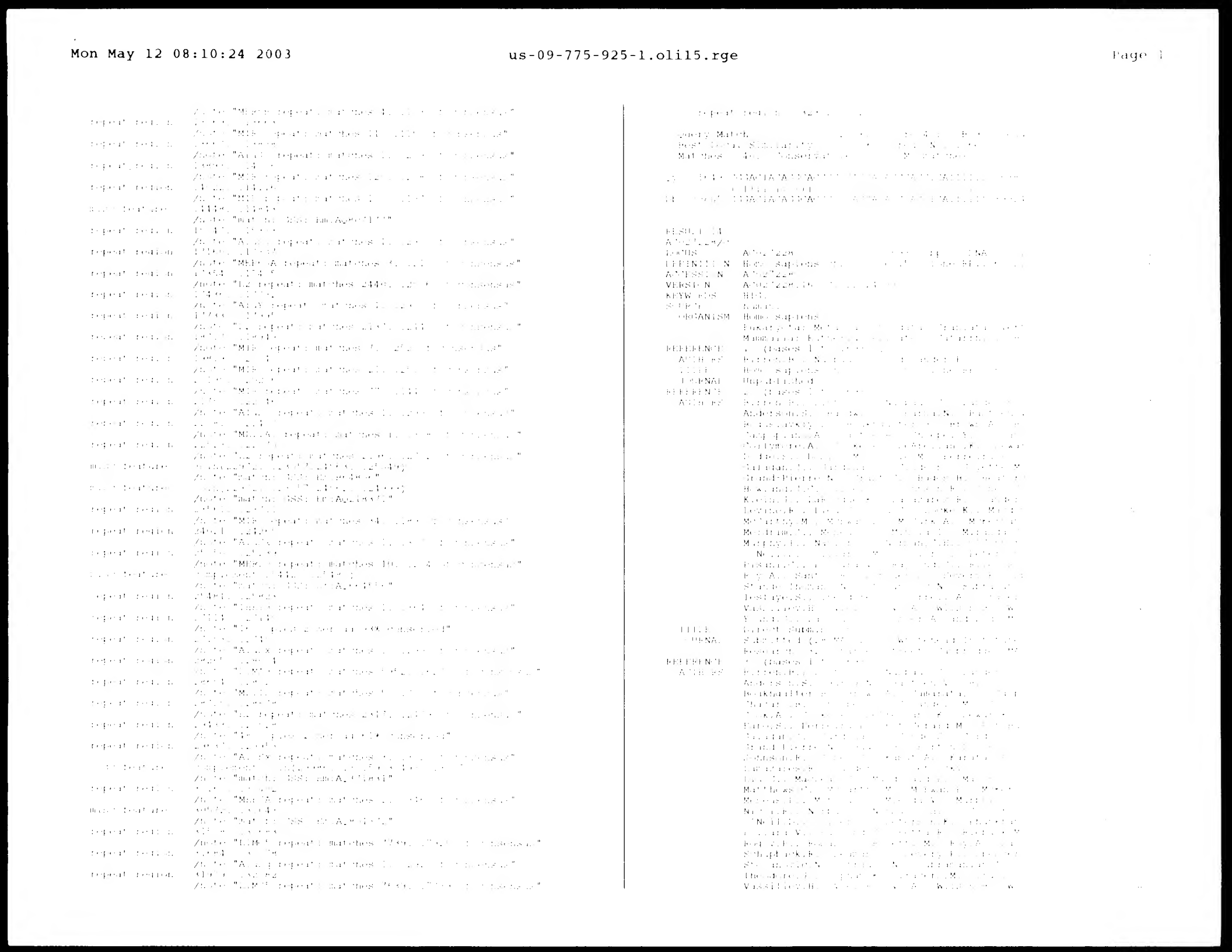

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            Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12 JUN 2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA [illegible] USA
REFERENCE   4  (bases 1 to 169377)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,[illegible]
            Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,[illegible]
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., [illegible]
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Gnirke,[illegible]
            Gardyna,S., Gord,S., Graham,L., Grand Pierre,N., Hagos,B.,
            Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
            Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
            Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,[illegible]
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,[illegible], Miranda,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Raymond,C., Rotta,K., Rise,C., Rogov,[illegible]
            Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
            Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., [illegible]
            Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., [illegible]
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31 JUL 2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   [illegible]  (bases 1 to 169377)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,[illegible]
            Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,[illegible]
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dooley,[illegible]
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Gnirke,[illegible]
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            Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
            Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,[illegible], Miranda,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
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            Phunkhang,P., Pierre,N., Raymond,C., Rotta,K., Rise,C., Rogov,P.,
            Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
            Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Thomas,[illegible]
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            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (09 AUG 2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
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                Contact: sequence_submissions@genome.wi.mit.edu
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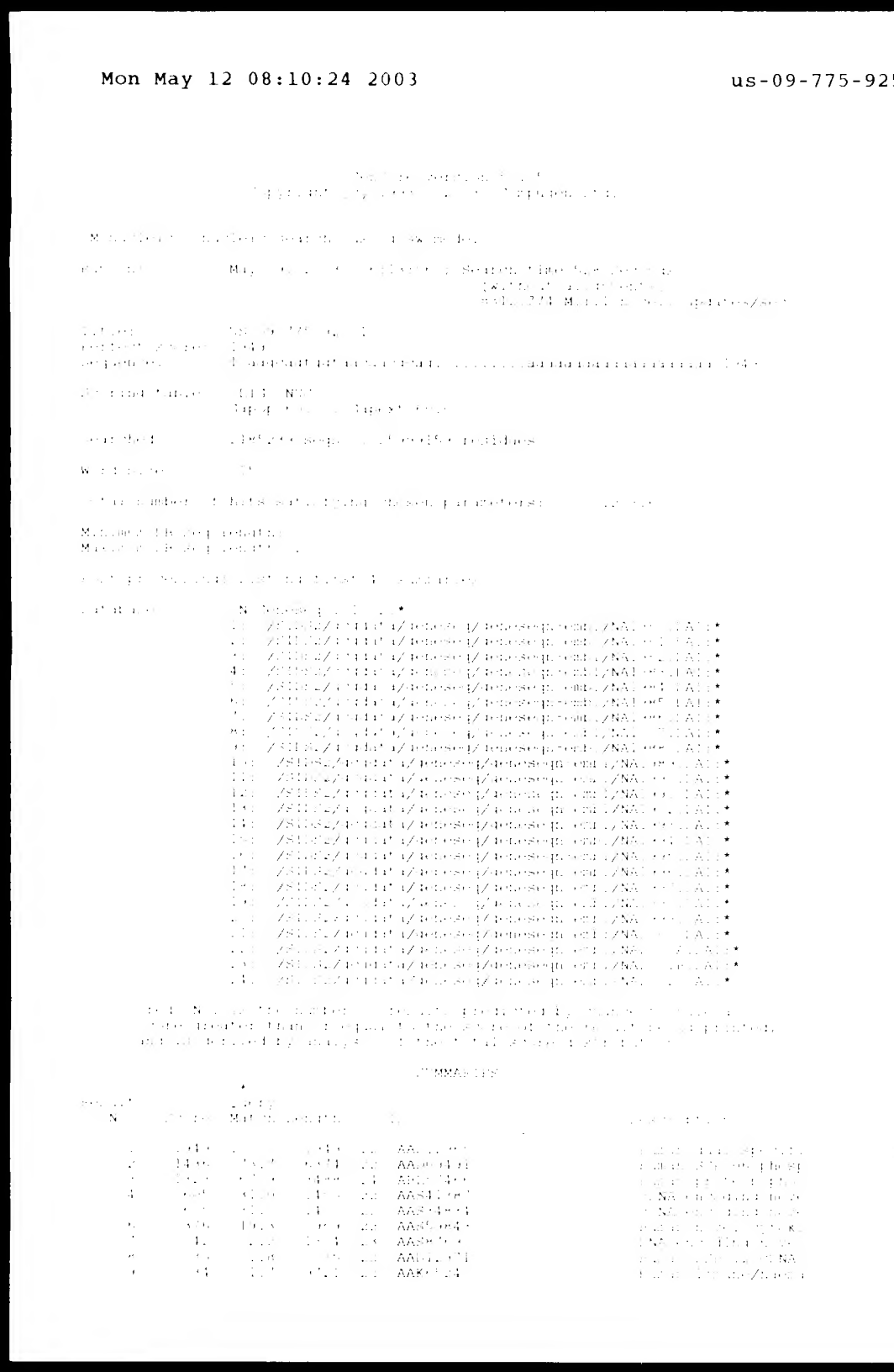

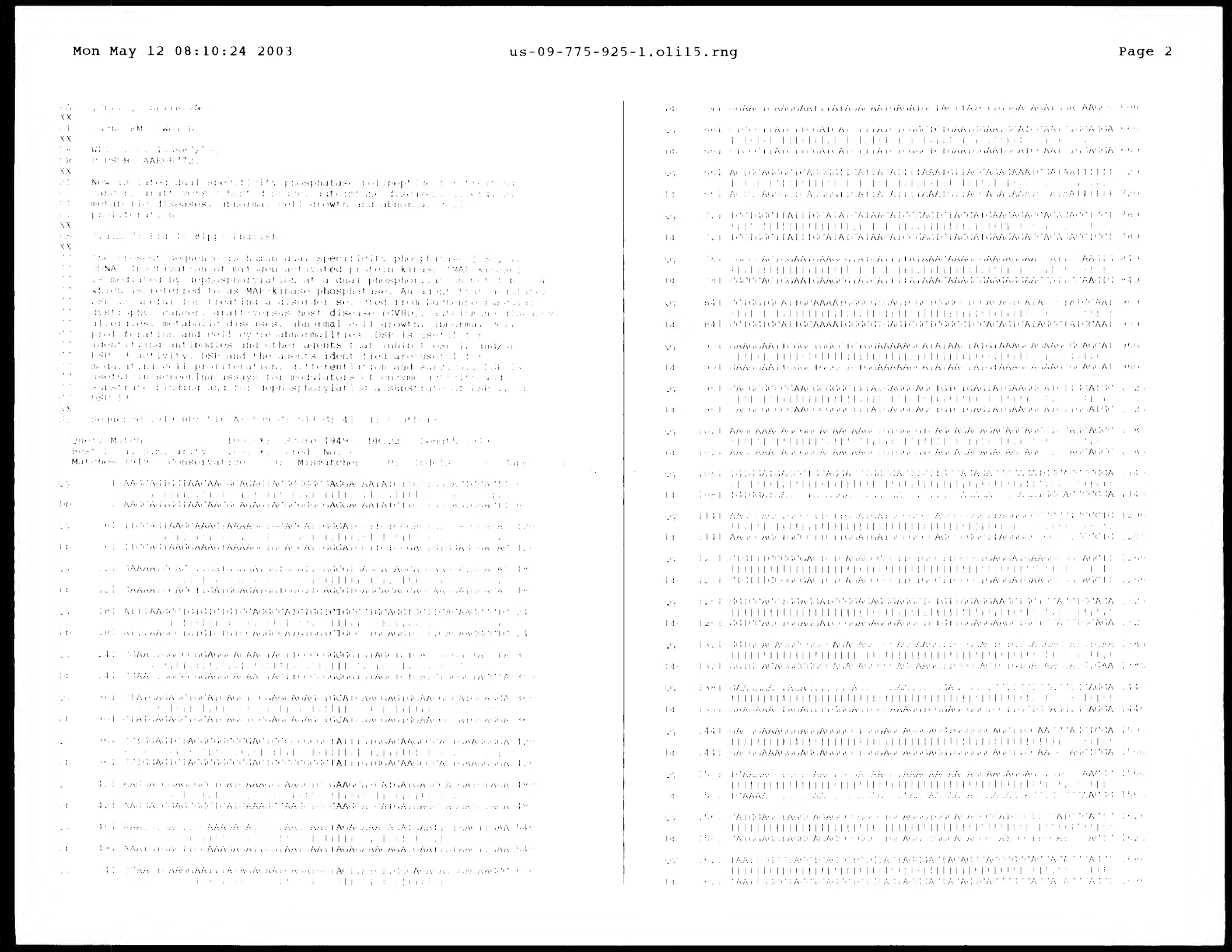

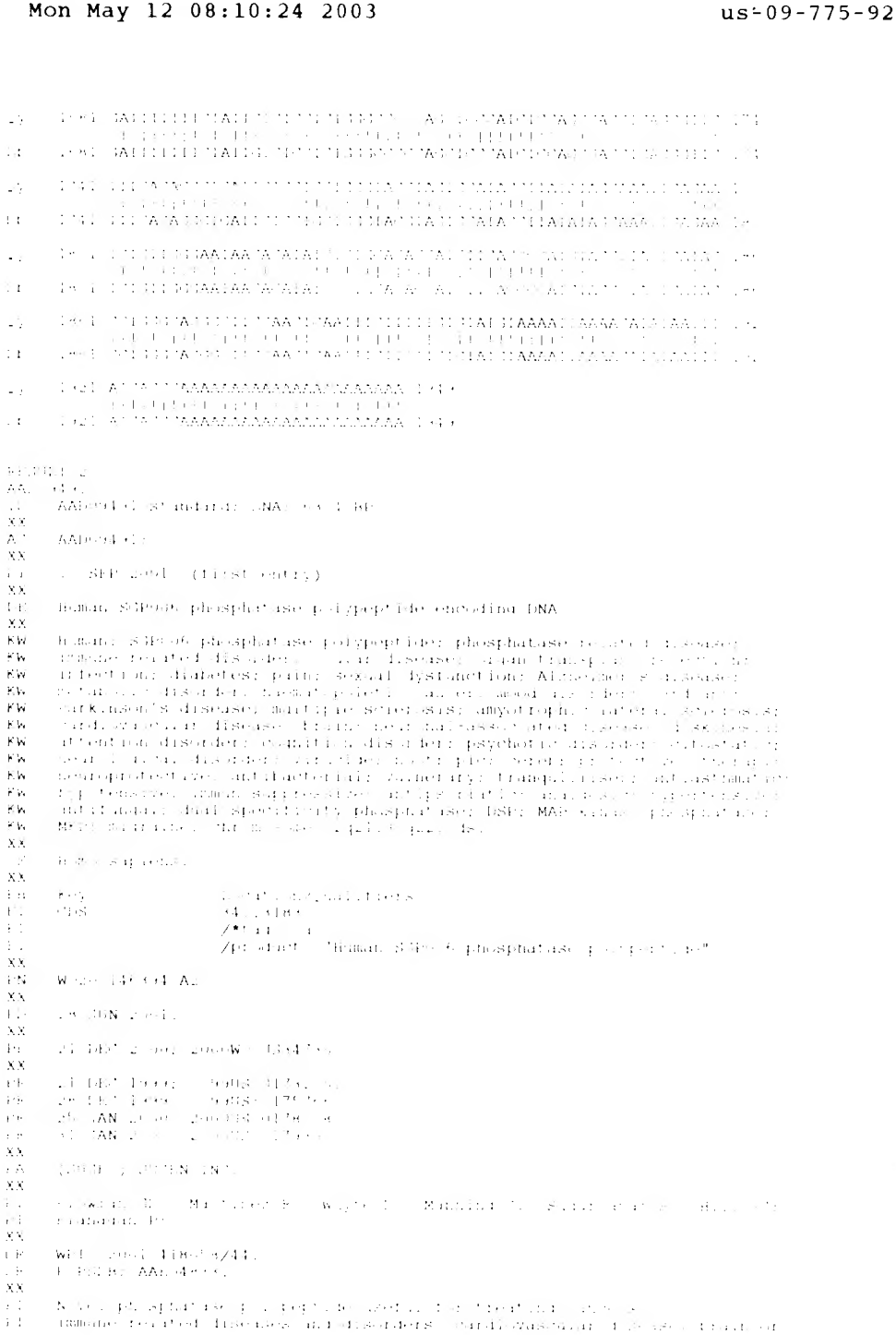

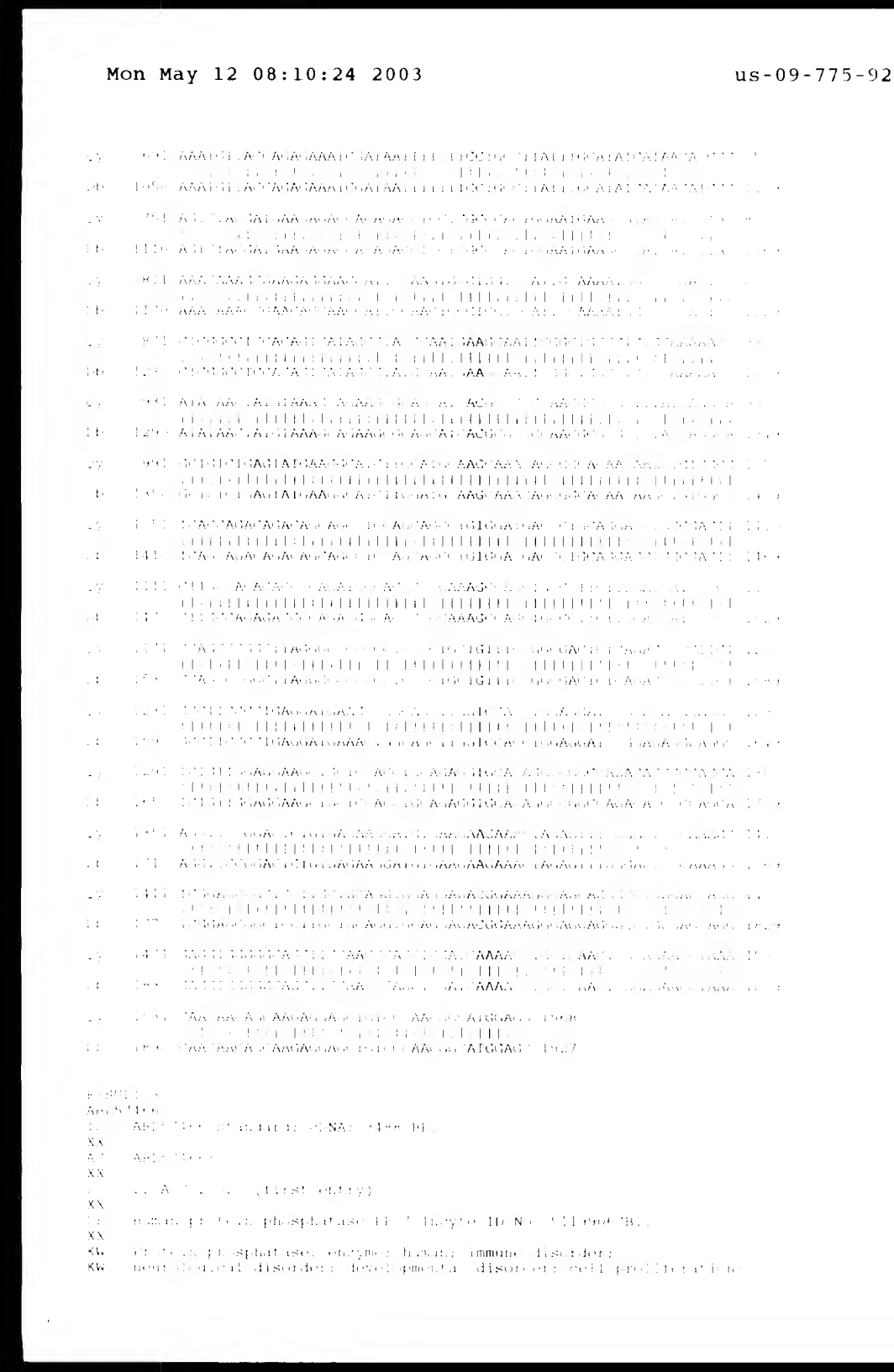

KW cancer; anti-HIV; antiallergic; antiasthmatic; antidiabetic; antifungal;
KW immunosuppressive; antipsoriatic; nootropic; antiparkinsonian;
KW antidepressant; antiosteoporotic; neuroprotective; antiarthritic;
KW hepatotropic; antiinflammatory; cytostatic; gene therapy; gene vac.
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OS Homo sapiens.
XX
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CC Claim 26 MAR 2002.
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PD 25-SEP-2001; 2001WO-US29451.
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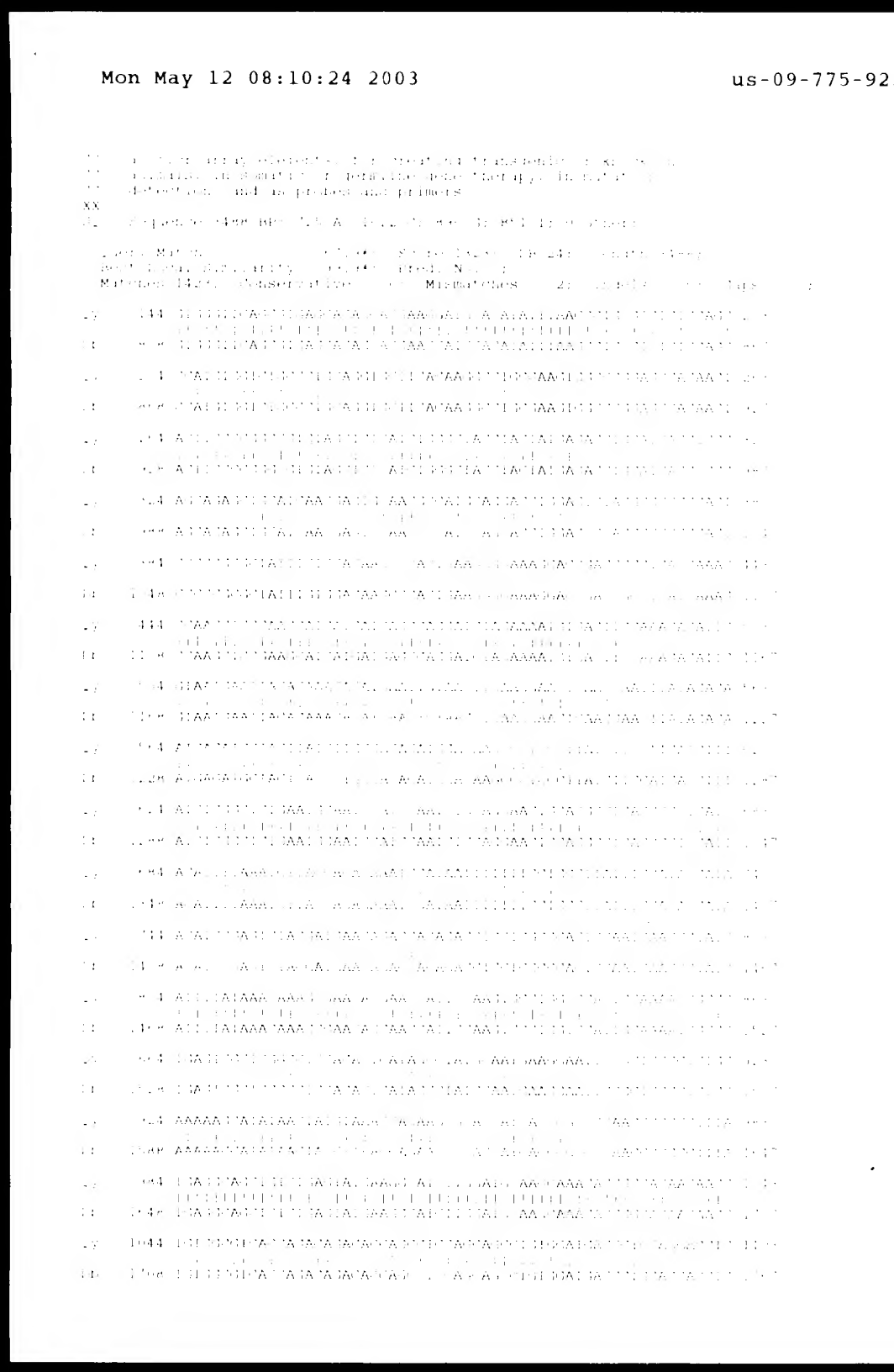
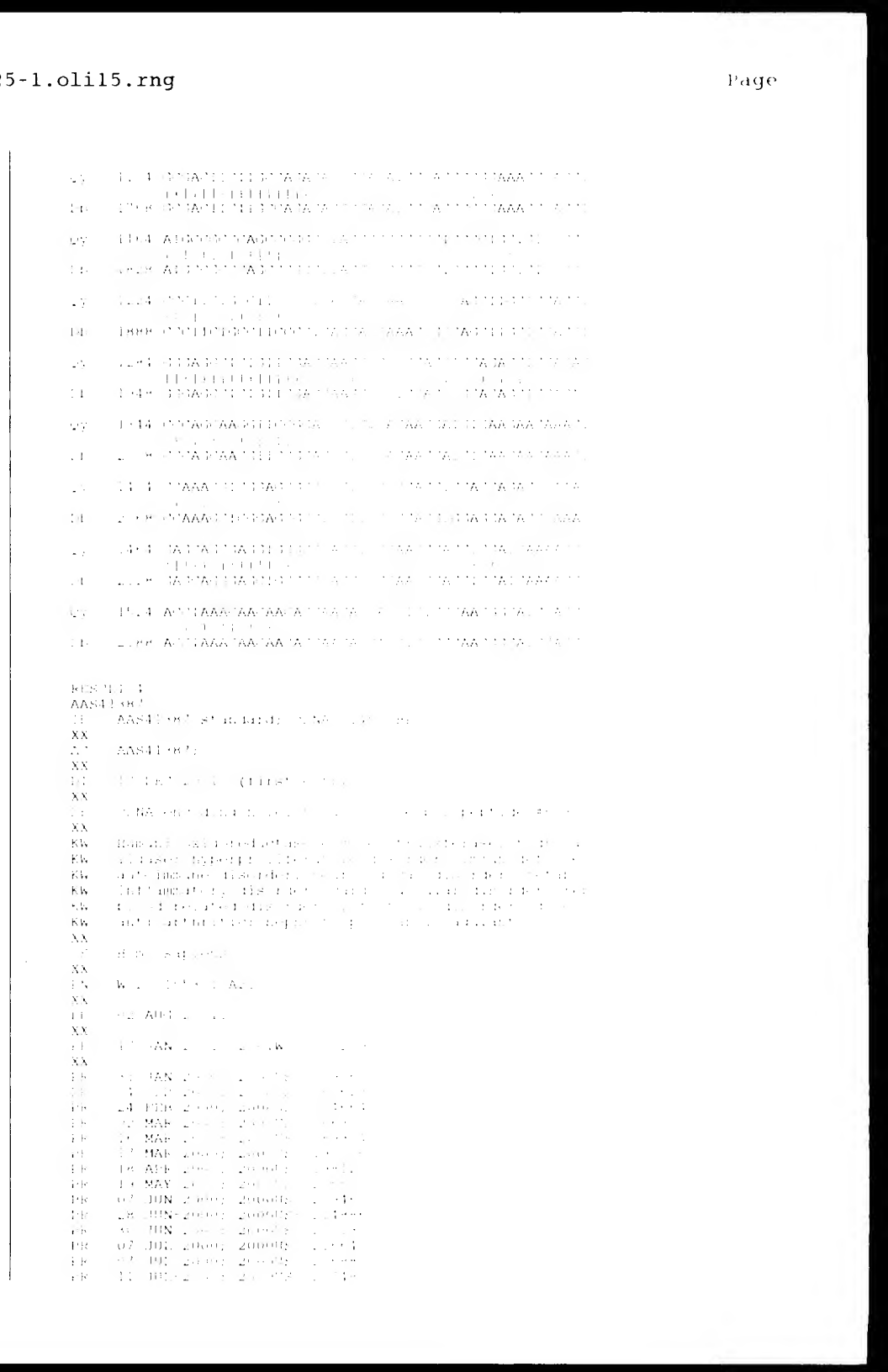
PR 25-SEP-2000; 2000US-235426P.
PR 29-SEP-2000; 2000US-236967P.
PR 06-OCT-2000; 2000US-238352P.
PR 19-OCT-2000; 2000US-242236P.
PR 27-OCT-2000; 2000US-243928P.
PR 17-NOV-2000; 2000US-249814P.
XX
PA (INCY) INCYTE GENOMICS INC.
XX
PI Ding YF, Yao MG, Walia NK, Elliott VS, Ramkumar J, Lu Y;
PI Arvizo C, Ding L, Baughn MR, Yue H, Lu DAM, Lubanski JM;
PI Thornton M, Gandhi AR, Lee EA, Xu Y, Wang YE, Bufalino ALA;
PI Rodriguez S, Daniels SE, Lal P, Swarnakar A;
XX
DR WPI; 2002-163755/43.
DR P-PSDB; AB876514.
XX
PT Novel human protein phosphatase polypeptides, useful in diagnosis,
PT prevention and treatment of immune disorders such as AIDS, neurological
PT disorders such as epilepsy, and developmental and cell proliferative
PT disorders
XX
PS Claim 5; Page 127 128; 1429pp; English.
XX
CC The present sequence is the nucleotide sequence of Incyte ID
CC 5119906CB1 encoding a novel protein phosphatase, designated PP 7
CC (see AAB76514). Putative protein phosphatases were initially
CC identified by running the Genscan gene identification program
CC against public genomic sequence databases. When necessary, the
CC predicted sequences were then edited to correct errors such as
CC extra or omitted exons. Full length polynucleotide sequences were
CC obtained by assembling predicted coding sequences with Incyte cDNA
CC sequence and/or public cDNA sequences, or were derived entirely
CC from edited or unedited Genscan predicted coding sequences. The
CC present sequence includes sequences obtained from several cDNA
CC libraries and from exons predicted from genomic DNA. A
CC representative library for the full length sequence is SMFCNOT1.
CC The encoded protein shows 97% identity to Drosophila MAP kinase
CC phosphatase and contains a dual specificity phosphatase catalytic
CC domain. The invention provides protein phosphatase PP 7 polypep-
CC tides, nucleic acids and polypeptides, expression vectors, host cells,
CC antibodies, agonists and antagonists. These are useful in the
CC diagnosis, treatment and prevention of disorders associated with
CC aberrant expression of protein phosphatase, including immune
CC system disorder (e.g. AIDS, Addison's disease, allergy, asthma,
CC atherosclerosis, multiple sclerosis, psoriasis), a neurological
CC disorder (e.g. Alzheimer's disease, Parkinson's disease, dementia,
CC depression, epilepsy, Tourette's disorder), developmental disorder
CC (e.g. renal tubular acidosis, myelodysplastic syndrome), and a cell
CC proliferative disorder (e.g. arteriosclerosis, cirrhosis,
CC neoplasms) including cancer. The nucleic acids are also useful





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PR 05 DEC 2000; 20000US 0251988.
PR 05-DEC 2000; 20000US 0256719.
PR 06-DEC-2000; 20000US 0251479.
PR 08 DEC-2000; 20000US-0251856.
PR 08 DEC-2000; 20000US-0251868.
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PR 08 DEC-2000; 20000US 0251989.
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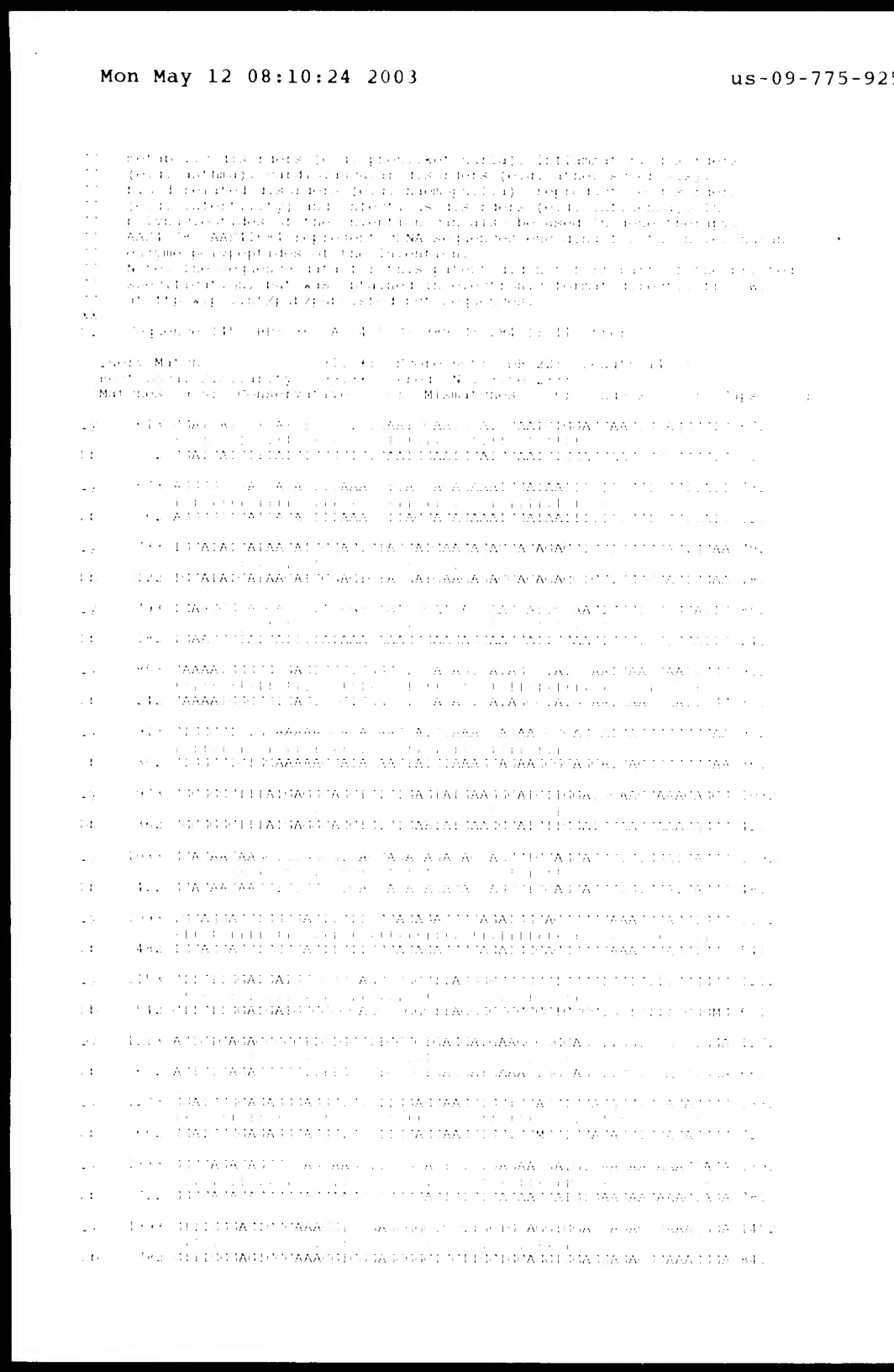
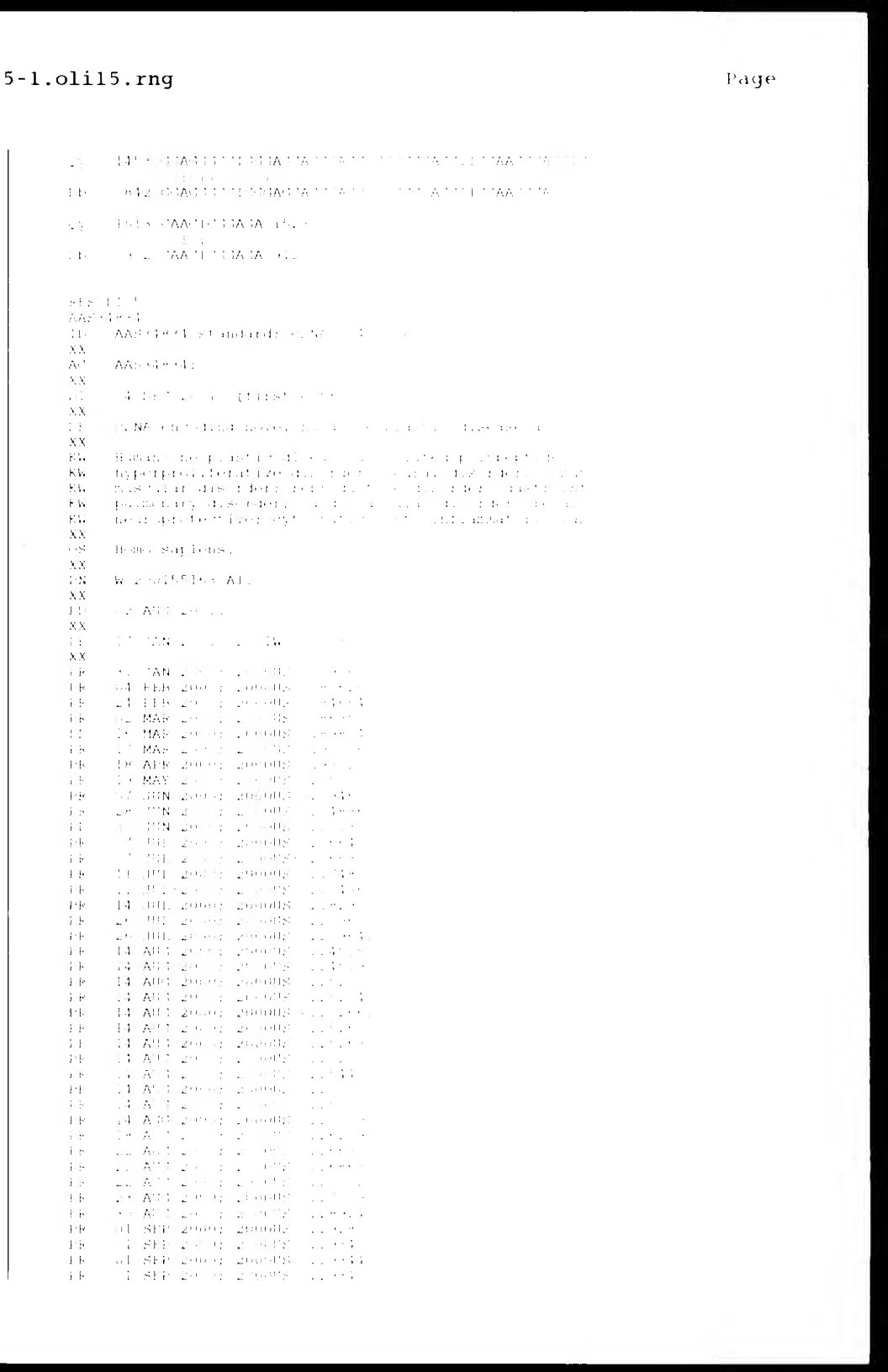
PR 11 DEC-2000; 20000US 0254097.
PR 05 JAN 2001; 20001US 0259678.
XX
PA (HUMA) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
DR P-PSDB; AAU23917.
XX
PT Novel polypeptides and polynucleotides useful for diagnostic,
PT preventing, treating neural, immune system, vascular, repr. biology,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases
XX
PS Claim 4; SEQ ID No 614; 1180pp. English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915 AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer), immune
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),





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PR 14 SEP 2000; 2000US-0243069.
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PR 15 SEP 2000; 2000US-0241228.
PR 21 SEP 2000; 2000US-0241274.
PR 25 SEP 2000; 2000US-0243997.
PR 25 SEP 2000; 2000US-0244098.
PR 26 SEP 2000; 2000US-0245484.
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PR 27 SEP 2000; 2000US-0245886.
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PR 29 SEP 2000; 2000US-0246697.
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PR 08 NOV 2000; 2000US-0247015.
PR 17 NOV 2000; 2000US-0249207.
PR 17 NOV 2000; 2000US-0249208.
PR 17 NOV 2000; 2000US-0249209.
PR 17 NOV 2000; 2000US-0249211.
PR 17 NOV 2000; 2000US-0249212.
PR 17 NOV 2000; 2000US-0249213.
PR 17 NOV 2000; 2000US-0249214.
PR 17 NOV 2000; 2000US-0249215.
PR 17 NOV 2000; 2000US-0249216.
PR 17 NOV 2000; 2000US-0249217.
PR 17 NOV 2000; 2000US-0249218.
PR 17 NOV 2000; 2000US-0249244.
PR 17 NOV 2000; 2000US-0249245.
PR 17 NOV 2000; 2000US-0249264.
PR 17 NOV 2000; 2000US-0249265.
PR 17 NOV 2000; 2000US-0249297.
PR 17 NOV 2000; 2000US-0249299.
PR 17 NOV 2000; 2000US-0249300.
PR 01 DEC 2000; 2000US-0250150.
PR 01 DEC 2000; 2000US-0250391.
PR 05 DEC 2000; 2000US-0251550.
PR 05 DEC 2000; 2000US-0251988.
PR 06 DEC 2000; 2000US-0256719.
PR 06 DEC 2000; 2000US-0251479.
PR 08 DEC 2000; 2000US-0257856.
PR 08 DEC 2000; 2000US-0251868.
PR 08 DEC 2000; 2000US-0251869.
PR 08 DEC 2000; 2000US-0251989.
PR 08 DEC 2000; 2000US-0251990.
PR 11 DEC 2000; 2000US-0254097.
PR 17 JAN 2001; 2001US-0259078.
XX
RA (HUMA) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-463598/50.
DR P-PSDB; AAG21665.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, and for treating cancers, neoplasia
PT arthritis
XX
PS Claim 4; SEQ ID NO 78; 68pp; English.
XX
CC The present invention relates to the isolation of novel human neoplastic
CC disease associated polypeptides (AAG21666-AAG21671), and DNA and RNA
CC sequences encoding for these polypeptides. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of disorders involving neoplastic disease such as
CC hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder
CC cancer, brain stem glioma, adult liver cancer, childhood cerebellar
CC astrocytoma, or Hodgkin's lymphoma). The sequences of the present invention
CC may be useful for treating other disorders such as neural disorders,
CC immune system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
CC and renal disorders. The polynucleotide sequences of the invention are
CC also useful in gene therapy. AAS34762-AAS34767 represent DNA sequences
CC encoding for the novel human neoplastic disease associated polypeptides
CC of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1450 BP; 360 A; 406 C; 689 G; 284 T; 11 other;

Query Match 31.0%; Score 60%; DB 22; Length 1450;
Best Local Similarity 99.8%; Pred. No. 3.5e-244;
Matches 965; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCGAGCCCCTTGCGCCTGGAGTTCCTCGCCGCCATCAACGACGCCGACCTGAAGAAG 60
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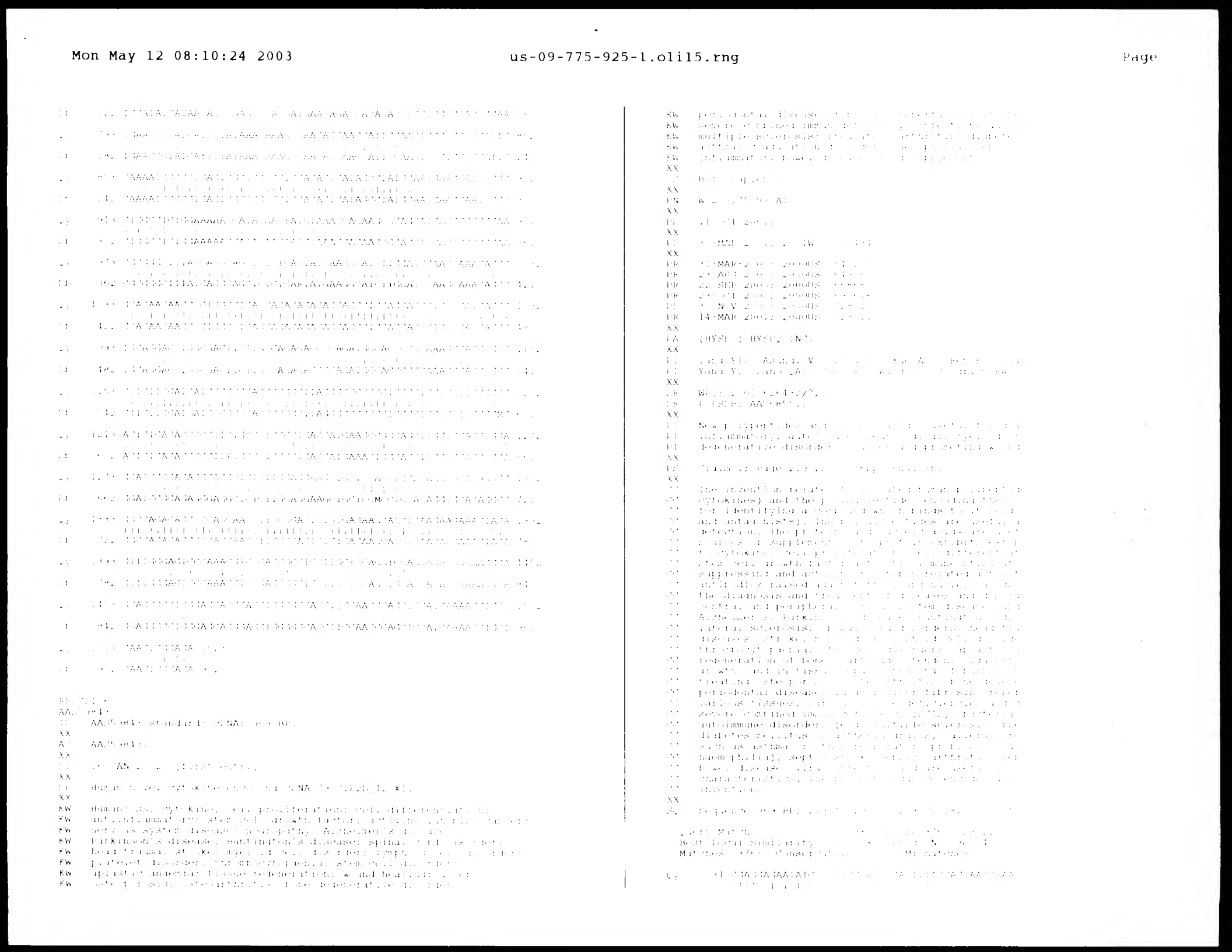
Db 1 ATGGCGAGCCCCTTGCGCCTGGAGTTCCTCGCCGCCATCAACGACGCCGACCTGAAGAAG 60

Qy 61 GCCCTCAAGGAGCTGGTGGACATCCTGGCCAAGAAGGAGAACAAGGCCGGCCAGGAGGTG 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GCCCTCAAGGAGCTGGTGGACATCCTGGCCAAGAAGGAGAACAAGGCCGGCCAGGAGGTG 120

Qy 121 GACGGCGACAACATCGCCGACAACGCCGCCAAGCAGATCGACCGCATCAACAAGTGGATGA 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GACGGCGACAACATCGCCGACAACGCCGCCAAGCAGATCGACCGCATCAACAAGTGGATGA 180



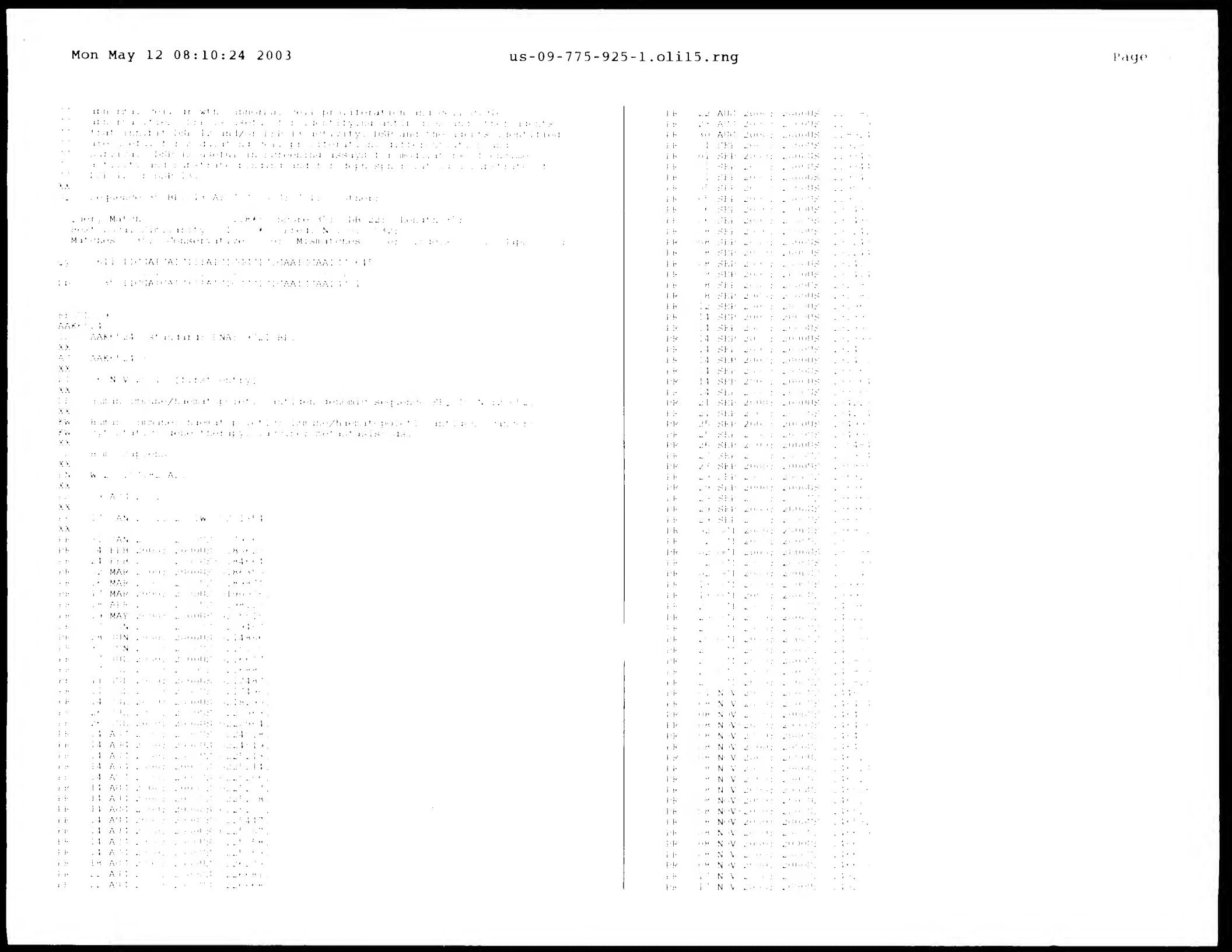
RESULT 7
AAS64564
ID AAS64564 standard; DNA; 45 BP.
XX
AC AAS64564;
XX
DT 15-FEB-2001 (first entry)
XX
DE DNA encoding novel human diagnostic protein #28494.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW blood supplement; medical imaging; diagnostic; genetic disorders; ss.
XX
OS Homo sapiens.
XX
PN WO200157221-A2.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US003429.
XX
PR 02-FEB-2000; 2000US-0179886.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Lal P, Wei GH;
XX
DR WPI; 2001-488887/53.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID NO 28494; 109pp; English.
XX
CC The present invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes
CC in Southern blot analysis (PCR) primers, probers, and to obtain or
CC map gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy to modulate
CC to restore normal activity of (II) or to treat disease states in which
CC (II). (II) is useful for generating antibodies against it. Note:

CC [continued] polypeptide is tissue, useful as blood cell markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64121-AAS64564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 BP; 315 A; 458 C; 325 G; 226 T; 0 other;

Query Match 2.2%; Score 42; DB 23; Length 1304;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 42
||||||||||||||||||||||||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 42

RESULT 8
AAS64121/c
ID AAS64121 standard; DNA; 45 BP.
XX
AC AAS64121;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human DSP 12 cDNA cloning and sequencing PCR primer (DSP12 SSP).
XX
KW Human; dual-specificity phosphatase; DSP-12; dual phosphorylation protein;
KW mitogen-activated protein kinase; MAP kinase; graft versus-host disease;
KW GVHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease;
KW allergy; metabolic disease; cell growth; cell proliferation; cytostatic;
KW cell cycle abnormality; cell differentiation; antiallergic; muscular;
KW immunosuppressive; RACE; rapid amplification of cDNA ends; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200157221-A2.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US003429.
XX
PR 02-FEB-2000; 2000US-0179886.
XX
PA (CHIR-) CHIRON INC.
XX
PI Luche RM, Wei H;
XX
DR WPI; 2001-488887/53.
XX
PT New isolated dual specificity phosphatase polypeptide for treating
PT cancer, graft versus host disease, autoimmune diseases, allergies,
PT metabolic diseases, abnormal cell growth and abnormal cell
PT proliferation
XX
PS Example 1; Page 42; 81pp; English.
XX
CC The present sequence is RACE (rapid amplification of cDNA ends) PCR
CC primer, DSP12-SSP3 used in the cloning and sequencing of human dual
CC specificity phosphatase (DSP) 12 cDNA. Inactivation of mitogen activated
CC protein kinase (MAP kinase) is mediated by dephosphorylation at a dual
CC phosphorylation motif by DSP which is referred to as MAP kinase
CC phosphatase. An agent that modulates DSP is useful for treating a
CC disorder selected from Duchenne muscular dystrophy, cancer, graft versus
CC host disease (GVHD), autoimmune diseases, allergies, metabolic [continued]



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PR 17 NOV 2000; 2000US0249211.
PR 17 NOV 2000; 2000US0249213.
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PR 17 NOV 2000; 2000US0249218.
PR 17 NOV 2000; 2000US0249244.
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PR 17 NOV 2000; 2000US0249267.
PR 17 NOV 2000; 2000US0249269.
PR 17 NOV 2000; 2000US0249406.
PR 01 DEC 2000; 2000US0256960.
PR 31 DEC 2000; 2000US0258067.
PR 05 DEC 2000; 2000US0251600.
PR 5 DEC 2000; 2000US0251608.
PR 5 DEC 2000; 2000US0256719.
PR 8 DEC 2000; 2000US0251479.
PR 08 DEC 2000; 2000US0251856.
PR 8 DEC 2000; 2000US0251868.
PR 08 DEC 2000; 2000US0251869.
PR 08 DEC 2000; 2000US0251889.
PR 08 DEC 2000; 2000US0251896.
PR 11 DEC 2000; 2000US0254007.
PR 05 JAN 2001; 2001US0259078.
XX
PA (BOMA) HUMAN GENOME SCI INC.
XX
PI Rosen CA; Barash SC; Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic action polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis
XX
PS Disclosure; SEQ ID NO 2002; 87pp; English.
XX
CC AAK64942 - AAK64943, encode the human immune/hematopoietic action (IA)
CC polypeptides. Full sequences range from AAM84170.1 - AAM84171.1, which
CC are useful, and can be used in gene therapy and vaccines to treat
CC cancers and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate IA expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by modifying mutations or deletions in a particular gene
CC that affect the activity of IA, by expressing inactive products that
CC suppress the activities of IA. Additionally, (1)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein; (2) proteins and polynucleotides may be used to present
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic derived cells. AAK64941
CC - AAK64941 represent human immune/haematopoietic amino acid
CC sequences from the present invention. AAK64942 to AAK64950 and AAM84170
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 87 BP; 22 A; 18 C; 19 G; 28 T; 0 U; 0 Other;

Query Match 1.7%; Score 62; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGTTAAAGTTCAAAAAAAAAAGTGATTTTT 62
|||||||||||||||||||||||||||||||
Db 26 AAAGTTAAAGTTCAAAAAAAAAAGTGATTTTT 87

RESULT 10

AAK64947
ID AAK64947 standard; DNA; 723 BP.
XX
AC AAK64947;
XX
DT 20-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic action gene sequence SEQ ID NO:2965.
XX
KW Human; immune; haematopoietic; immune/haematopoietic action; cancer;
KW metastasis; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
CN WO200179482-A2.
XX
PD 25-OCT-2001.
XX
PF 17-JAN-2001; 2001WO-US01454.
XX
PR 17-JAN-2000; 2000US-0176965.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184964.
PR 02-MAR-2000; 2000US-0186450.
PR 10-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190976.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 29-JUN-2000; 2000US-0215145.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 13-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217996.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220663.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224579.
PR 14-AUG-2000; 2000US-0225215.
PR 14-AUG-2000; 2000US-0225274.
PR 14-AUG-2000; 2000US-0225566.
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PR 14-AUG-2000; 2000US-0225571.
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PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225774.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226869.
PR 23-AUG-2000; 2000US-0227092.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228944.
PR 01-SEP-2000; 2000US-0229287.
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PR 01-SEP-2000; 2000US-0229444.
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PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230498.
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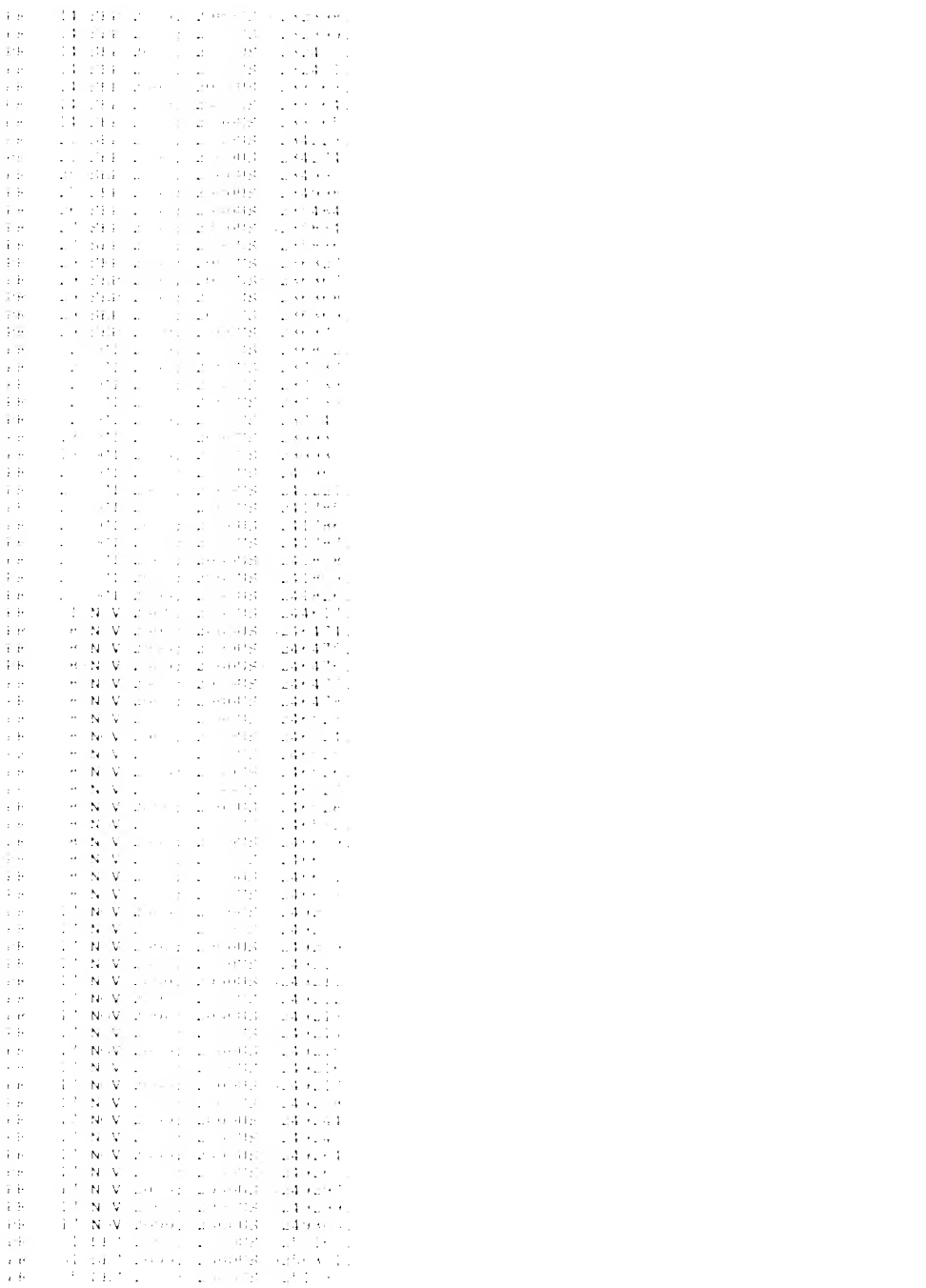
PR 08-SEP-2000; 2000US-0231253.
PR 08-SEP-2000; 2000US-0231254.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231434.
PR 08-SEP-2000; 2000US-0232089.
PR 08-SEP-2000; 2000US-0232091.
PR 12-SEP-2000; 2000US-0231908.
PR 14-SEP-2000; 2000US-0232297.



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XX
DT   27-MAY-[illegible] (rel. [illegible], Created)
XX
DT   27-MAY-[illegible] (rel. [illegible], Last updated, Version [illegible])
XX
DE   [illegible] GENOME THERAPEUTICS CORP.
RA   (UYCK ) UNIV CHEICHEN CHEN'S MED.COLLEGE.
XX
RA   Carulli JP, Little RD, Booker RR, Johnson ML;
XX
RT   WO [illegible]/[illegible].
XX
PT   Identifying molecules involved in lipid regulation, useful for
PT   diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT   identifying a molecule that binds to high bone mass gene or its
PT   corresponding wild type gene.
XX
PS   Example 2; Page 320-322; 409pp; English.
XX
CC   The invention relates to a method for identifying a molecule involved in
CC   lipid regulation comprising identifying a molecule that binds to or
CC   inhibits binding of a molecule to high bone mass (HBM) or it's wild type
CC   gene, Zmax1. Compounds identified by the method are useful for treating,
CC   diagnosing, preventing or screening for normal and abnormal
CC   lipid associated conditions, including arteriosclerosis, cardiovascular
CC   disease, stroke, and osteoporosis. The compounds may also be used in the
CC   treatment or prevention of diabetic atherosclerosis, poor vascular
CC   conditions caused by plaque build up, poor circulation due to plaque
CC   build up and associated poor wound healing. The methods can be used in
CC   gene therapy, pharmaceutical development, and diagnostic assays for bone
CC   development disorders. Molecules identified by comparison of Zmax1 and
CC   HBM systems can be used as surrogate markers in pharmaceutical
CC   development, in diagnosis of human or animal bone disease, and in the
CC   treatment of bone diseases. Sequences ABK22776 ABK22841 represent cDNA
CC   molecules encoding human Zmax1 and HBM, and PCR primers, probes, vectors
CC   and adapters of the invention.
XX
SQ   Sequence 57273 BP; 12179 A; 15326 C; 15607 G; 14161 T; 0 other;

  Query Match                 1.7%;  Score 34;  DB 24;  Length 57273;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGATAACGAACGCGCAGCAGAGCGAATGAATTT 34
           ||||||||||||||||||||||||||||||||||
Db   25700 GATAAGCACGCGCCACGACAGCCAGCTGAATTTT 25667


RESULT 2
ABAB62625
ID   ABAB62625 standard; DNA; 60333 BP.
XX
AC   ABAB62625;
XX
DT   25-JAN-2002  (first entry)
XX
DE   Human HBM gene region bz0602f h_con'144.
XX
KW   Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW   sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW   antisense therapy; vaccine; bone disorder; Paget's disease;
KW   osteosclerosis; osteomalacia; fibrous dysplasia; ds.
XX
OS   Homo sapiens.
XX
FN   WO200177627-A1.
XX
PD   18-OCT-2001.
XX
PF   11-JAN-2000; 2000WO-US00951.
XX
PR   05-APR-2000; 2000US-0544777.
PR   05-APR-2000; 2000US-0544869.
XX
PA   (GENE ) GENOME THERAPEUTICS CORP.
```

```
XX
[illegible]
XX
PN   W[illegible]
XX
PT   New high bone mass (HBM) and [illegible] genes and proteins [illegible]
PT   modulating bone mass [illegible] the treatment [illegible]
XX
PS   [illegible] 44[illegible]pp; English.
XX
CC   The present invention describes the human [illegible] gene [illegible] high bone
CC   mass (HBM) gene which [illegible]
CC   HBM genes have [illegible] The genes [illegible]
CC   therapy, antisense therapy and in the production [illegible]
CC   can be used in the [illegible] and treatment [illegible]
CC   [illegible]
CC   dysplasia. ABA[illegible] ABA[illegible] AA[illegible] AA[illegible]
CC   sequences used in the exemplification of the present [illegible]
XX
SQ   Sequence [illegible] BP; [illegible]

  Query Match [illegible] Score [illegible] DB [illegible] Length [illegible]
  Best Local Similarity [illegible] Pred. No. [illegible]
  Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

Qy   [illegible] [illegible]A[illegible]A[illegible]A[illegible]A[illegible] [illegible]

Db   [illegible] [illegible]A[illegible]A[illegible]A[illegible]A[illegible] [illegible]


RESULT [illegible]
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ID   ABA[illegible] standard; DNA; [illegible]
XX
AC   ABA[illegible]
XX
DT   [illegible] JAN 2002 (first entry)
XX
DE   Human HBM gene [illegible]
XX
KW   Human; high bone mass; HBM gene; [illegible] gene; [illegible]
KW   [illegible] osteoporosis; osteopath[illegible] therapy;
KW   antisense therapy; [illegible] disorder; [illegible]
KW   [illegible] dysplasia; [illegible]
XX
OS   Homo sapiens.
XX
PN   W[illegible] A[illegible]
XX
PD   [illegible]
XX
PF   [illegible] JUN 2000; 2000W[illegible]
XX
PR   [illegible] APR [illegible]
PR   [illegible] APR [illegible]
XX
PA   ([illegible]) [illegible]
XX
PI   [illegible]
XX
DR   W[illegible]
XX
PT   New high bone mass (HBM) [illegible] genes and proteins [illegible]
PT   modulating bone mass [illegible] the treatment [illegible]
XX
PS   [illegible] 44[illegible]pp; English.
XX
CC   The present invention describes the human [illegible] gene [illegible] high bone
CC   mass (HBM) gene, which are found on chromosome 11q[illegible]
CC   HBM genes have [illegible] The genes [illegible]
CC   therapy, antisense therapy and in the production [illegible]
CC   can be used in the [illegible] and treatment [illegible]
CC   [illegible]
CC   dysplasia. ABA[illegible] AA[illegible]
CC   sequences used in the [illegible]
XX
SQ   Sequence [illegible] BP; [illegible]

  Query Match [illegible]
  Best Local Similarity [illegible]
  Matches [illegible] Conservative [illegible] Mismatches [illegible]

Qy   [illegible] [illegible]A[illegible]A[illegible] [illegible]

Db   [illegible] [illegible]A[illegible]A[illegible] [illegible]


RESULT [illegible]
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ID   AAS[illegible] standard; DNA; [illegible]
XX
AC   AAS[illegible]
XX
DT   [illegible] DEC 200[illegible] (first entry)
XX
DE   Human DNA [illegible] SEQ ID NO [illegible]
XX
KW   Human; foetal tissue; [illegible]
KW   [illegible]
KW   cardi[illegible]
KW   hyperproliferative [illegible]
KW   cardiovascular disorder; [illegible]
KW   [illegible]
KW   Alzheimer's disease; [illegible]
KW   [illegible]
XX
OS   Homo sapiens.
XX
PN   W[illegible] A2.
XX
PD   [illegible] AUG 200[illegible]
XX
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PR 17 NOV 2000; 200000S 0249213.
PR 17 NOV 2000; 200000S 0249214.
PR 17 NOV 2000; 200000S 0249215.
PR 17 NOV 2000; 200000S 0249216.
PR 17 NOV 2000; 200000S 0249217.
PR 17 NOV 2000; 200000S 0249218.
PR 17 NOV 2000; 200000S 0249244.
PR 17 NOV 2000; 200000S 0249245.
PR 17 NOV 2000; 200000S 0249264.
PR 17 NOV 2000; 200000S 0249265.
PR 17 NOV 2000; 200000S 0249267.
PR 17 NOV 2000; 200000S 0249269.
PR 17 NOV 2000; 200000S 0249330.
PR 01 DEC 2000; 200000S 0250160.
PR 01 DEC 2000; 200000S 0250891.
PR 05 DEC 2000; 200000S 0251030.
PR 05 DEC 2000; 200000S 0251988.
PR 06 DEC 2000; 200000S 0252119.
PR 06 DEC 2000; 200000S 0251479.
PR 08 DEC 2000; 200000S 0251870.
PR 08 DEC 2000; 200000S 0251868.
PR 08 DEC 2000; 200000S 0251869.
PR 08 DEC 2000; 200000S 0251989.
PR 08 DEC 2000; 200000S 0251990.
PR 11 DEC 2000; 200000S 0254097.
PR 05 JAN 2001; 206JUS 0259678.
XX
PA (BRMA) BRITISH COLUMBIA SCI ANC.
XX
PI Bosch PA, Barash SC, Pubic SM;
XX
DR WPI; 2001-188782/54.
XX
PT New polynucleotides and polypeptides for diagnosing, treating,
PT preventing or prognosing e.g. diseases or disorders of the nervous,
PT musculoskeletal, excretory, gastrointestinal, reproductive and
PT respiratory systems
XX
PS Disclosure; SEQ ID No 1869; 64pp; English.
XX
CC The invention relates to novel nucleic acids encoding cancer, brain tumor
CC antigens. The nucleic acids and proteins are used to prevent, treat (e.g.
CC by gene therapy) or ameliorate a medical condition (e.g. tumors, cancers,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. The antibodies to the antigens can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme-linked
CC immunosorbent assays (ELISA). Disorders which are treated and/or
CC diagnosed include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, atherosclerosis, nervous system disorders e.g.
CC Alzheimer's disease, infectious caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs fed to
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. Note: not
CC examples of diseases and disorders treated by the nucleic acids and
CC proteins are given in the specification. The present sequence
CC is a genomic DNA fragment from a gene encoding a foetal antigen of the

Query Match 1.9%; Score 32; DB 22; Length 2?3;
Best Local Similarity 100.0%; Pred. No. 6.e+02;

SUMMARIES

Result No.	Score	Match Length	DB	ID	Description
1	715	99.7	11	BM47...27	BM47...27 AGEN...
2	690	96.2	11	BM...34...	BM...34... ......
3	683	28.4	10	BM71...00	BM...... ......
4	673	28.1	11	BM......	BM...... AGEN...
5	647	28.0	10	AF113...3	AF113...3 BM21...27
6	644	28.0	10	BM21...43	BM21...43 ......
7	644	28.0	10	BM21...43	BM21...43 ......
8	644	28.0	10	BM21...43	BM21...43 ......
9	644	28.0	10	BM21...43	BM21...43 ......
10	644	28.0	10	BM21...43	BM21...43 ......
11	644	28.0	10	BM21...43	BM21...43 ......
12	644	28.0	10	BM21...43	BM21...43 ......
13	644	28.0	10	BM21...43	BM21...43 ......
14	644	28.0	10	BM21...43	BM21...43 ......
15	644	28.0	10	BM21...43	BM21...43 ......
16	644	28.0	10	BM21...43	BM21...43 ......
17	644	28.0	10	BM21...43	BM21...43 ......
18	644	28.0	10	BM21...43	BM21...43 ......
19	644	28.0	10	BM21...43	BM21...43 ......
20	644	28.0	10	BM21...43	BM21...43 ......
21	644	28.0	10	BM21...43	BM21...43 ......
22	644	28.0	10	BM21...43	BM21...43 ......
23	644	28.0	10	BM21...43	BM21...43 ......
24	644	28.0	10	BM21...43	BM21...43 ......
25	644	28.0	10	BM21...43	BM21...43 ......
26	644	28.0	10	BM21...43	BM21...43 ......
27	644	28.0	10	BM21...43	BM21...43 ......
28	644	28.0	10	BM21...43	BM21...43 ......
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40	644	28.0	10	BM21...43	BM21...43 ......
41	644	28.0	10	BM21...43	BM21...43 ......
42	644	28.0	10	BM21...43	BM21...43 ......
43	644	28.0	10	BM21...43	BM21...43 ......
44	644	28.0	10	BM21...43	BM21...43 ......
45	644	28.0	10	BM21...43	BM21...43 ......

ALIGNMENTS

RESULT 1
BM47...27
LOCUS BM47...27 ... bp ... DNA ...
DEFINITION AGENCOURT ... Sus scrofa ... mRNA sequence.
ACCESSION BM47...27
VERSION BM47...27.1 ...
KEYWORDS EST.
SOURCE Domestic ...
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; ...
Mammalia; Eutheria; Laurasiatheria; Artiodactyla; ...
REFERENCE 1 (bases ... to ...)
AUTHORS NIH MGC ...
TITLE NIH Mammalian Gene Collection (MGC) Mammalian ...
JOURNAL Unpublished ...
COMMENT Contact: MGC ...
Clone distribution: ...
Clone distribution: MGC ... no distribution ...
Seq primer: ...
Library ...
Plate: CLAM... ...
High quality ...
High quality ...
FEATURES ...

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SOURCE          1..1121
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                /db_xref "taxon:9606"
                /clone "IMAGE:3544482"
                /clone_lib "NIH_MGC_71"
                /tissue_type "leiomyosarcoma"
                /lab_host "DH10B (phage resistant)"
                /note "Organ: uterus; Vector: pCMV [illegible] Site 2: SalI; Cloned unidirectionally. [illegible]
                Average insert size 2.1 kb [illegible]"
BASE COUNT      [illegible] a   279 c   [illegible] g   [illegible] t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches  715;  Conservative    0;  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        180 [illegible]
Db        140 [illegible]

Qy        240 [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        400 [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        480 [illegible]
Db        440 [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible] 724
Db        [illegible]

RESULT [illegible]
BM[illegible]
LOCUS       BM[illegible]          640 bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] Homo sapiens cDNA [illegible]
            [illegible] mRNA sequence.
ACCESSION   BM[illegible]
VERSION     BM[illegible]

KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@[illegible]uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            The following repetitive elements were found in this cDNA
            sequence: 259-318, [illegible]
            Seq primer: M13 Forward
            POLYA Yes.
FEATURES             Location/Qualifiers
     source          1..640
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                     /db_xref "taxon:9606"
                     /clone "UI-E-EJ0-ahj-k-16-0-UI"
                     /clone_lib "UI-E-EJ0"
                     /tissue_type "fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage "fetal and adult"
                     /lab_host "DH10B (Life Technologies) (T1 phage resistant)"
                     /note "Organ: eye; Vector: pT7T3 Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     UI-E-EJ0 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, A[illegible]
                     ; lens, [illegible]; eye anterior segment, [illegible]
                     optic nerve, [illegible]; retina, [illegible]; Retina Foveal and
                     Macular, [illegible]
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI).
                     TAG_LIB UI-E-EJ0
                     TAG_TISSUE RPE and Choroid
                     TAG_SEQ ACTTA"
BASE COUNT      136 a    160 c    171 g    172 t      1 others
ORIGIN

  Query Match             [illegible]%;  Score 588;  DB 14;  Length 640;
  Best Local Similarity   [illegible]%;  Pred. No. 0;
  Matches  639;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1306 [illegible] 1365
Db        640 [illegible]

Qy       [illegible] 1425
Db        581 [illegible] 521
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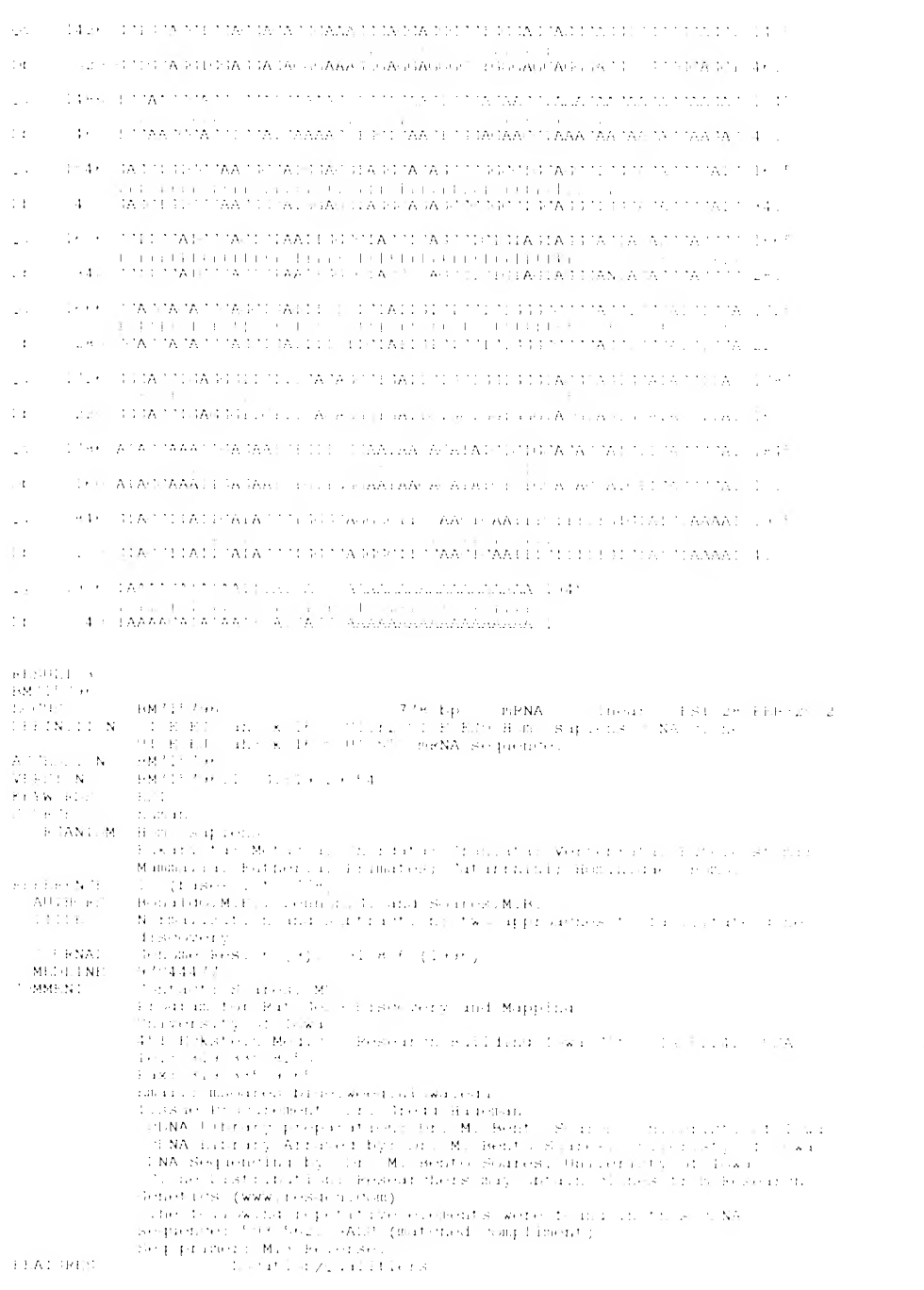

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RESULT 4
AM762224.3
LOCUS       AM762224                 596 bp    mRNA    linear   EST 25-FEB-2003
DEFINITION  DKFZp762C027 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762C027 3', mRNA sequence.
ACCESSION   AM762224
VERSION     AM762224.3  GI:68344474
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 596)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     EST (Ottenwaelder, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Ottenwaelder B
            MIPS
            Am Klopferspitz 18a D 82152 Martinsried, Germany
            This is the 3' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
            sequenced by MediGenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project; 2 sequences
            also available.
            This clone (DKFZp762C027) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcencentrum, Bezugsweg 7, D 14 5
            Berlin, Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1..596
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762C027"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site 1: Not1; Site 2: Sal1"
BASE COUNT      127 a    168 c    168 g    242 t
ORIGIN

  Query Match             28.0%;  Score 546;  DB 9;  Length 596;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  546;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAATTTTAATTTTGGATTTTTTTTTTAATTTGGTAGGAGTAGTAAAAAAAAAAAAAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAAATTTTAATTTTGGATTTTTTTTTTAATTTGGTAGGAGTAGTAAAAAAAAAAAAAAA 60

Qy         61 AAAAAGCAAGCTCGGAAGCATCATCATGAGGCAGGATTATGAAAATGTGATTTGCAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAAGCAAGCTCGGAAGCATCATCATGAGGCAGGATTATGAAAATGTGATTTGCAAA 120

Qy        121 GACATTCGTAATGAATTAGAGAAACAGATGAATTGTAACTTGAAGGAACTCTAACTAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACATTCGTAATGAATTAGAGAAACAGATGAATTGTAACTTGAAGGAACTCTAACTAATTT 180

Qy        181 ....AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT 240

Qy        241 AAAATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 300

Qy        301 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360

Qy        361 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 420

Qy        421 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 480

Qy        481 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 540

Qy        541 TTTTTT 546
              ||||||
Db        541 TTTTTT 546


RESULT 5
AM762224/c
LOCUS       AM762224                 596 bp    mRNA    linear   EST 25-FEB-2003
DEFINITION  DKFZp762C027 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762C027 3', mRNA sequence.
ACCESSION   AM762224
VERSION     AM762224.3  GI:68344474
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 596)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     EST (Ottenwaelder, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Ottenwaelder B
            MIPS
            Am Klopferspitz 18a D 82152 Martinsried, Germany
            This is the 3' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
            sequenced by MediGenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project; 2 sequences
            also available.
            This clone (DKFZp762C027) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcencentrum, Bezugsweg 7, D 14 5
            Berlin, Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1..596
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762C027"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site 1: Not1; Site 2: Sal1"
BASE COUNT      127 a    168 c    168 g    242 t
ORIGIN

  Query Match             28.0%;  Score 546;  DB 9;  Length 596;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  546;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAATTTTAATTTTGGATTTTTTTTTTAATTTGGTAGGAGTAGTAAAAAAAAAAAAAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAAATTTTAATTTTGGATTTTTTTTTTAATTTGGTAGGAGTAGTAAAAAAAAAAAAAAA 60

Qy         61 AAAAAGCAAGCTCGGAAGCATCATCATGAGGCAGGATTATGAAAATGTGATTTGCAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAAGCAAGCTCGGAAGCATCATCATGAGGCAGGATTATGAAAATGTGATTTGCAAA 120

Qy        121 GACATTCGTAATGAATTAGAGAAACAGATGAATTGTAACTTGAAGGAACTCTAACTAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACATTCGTAATGAATTAGAGAAACAGATGAATTGTAACTTGAAGGAACTCTAACTAATTT 180

Qy        181 ....AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT 240

Qy        241 AAAATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 300

Qy        301 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360

Qy        361 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 420

Qy        421 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 480

Qy        481 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 540

Qy        541 TTTTTT 546
              ||||||
Db        541 TTTTTT 546
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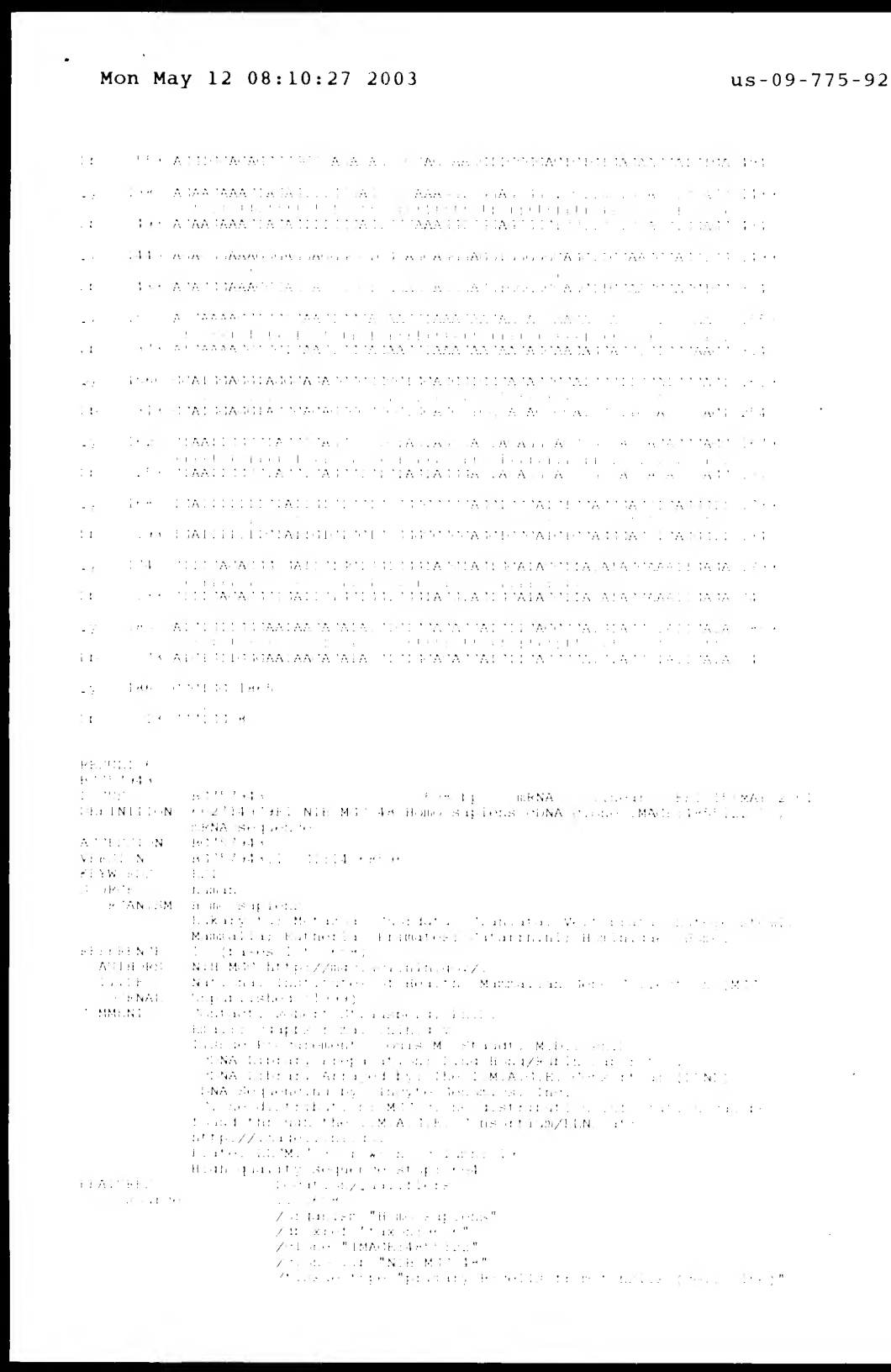

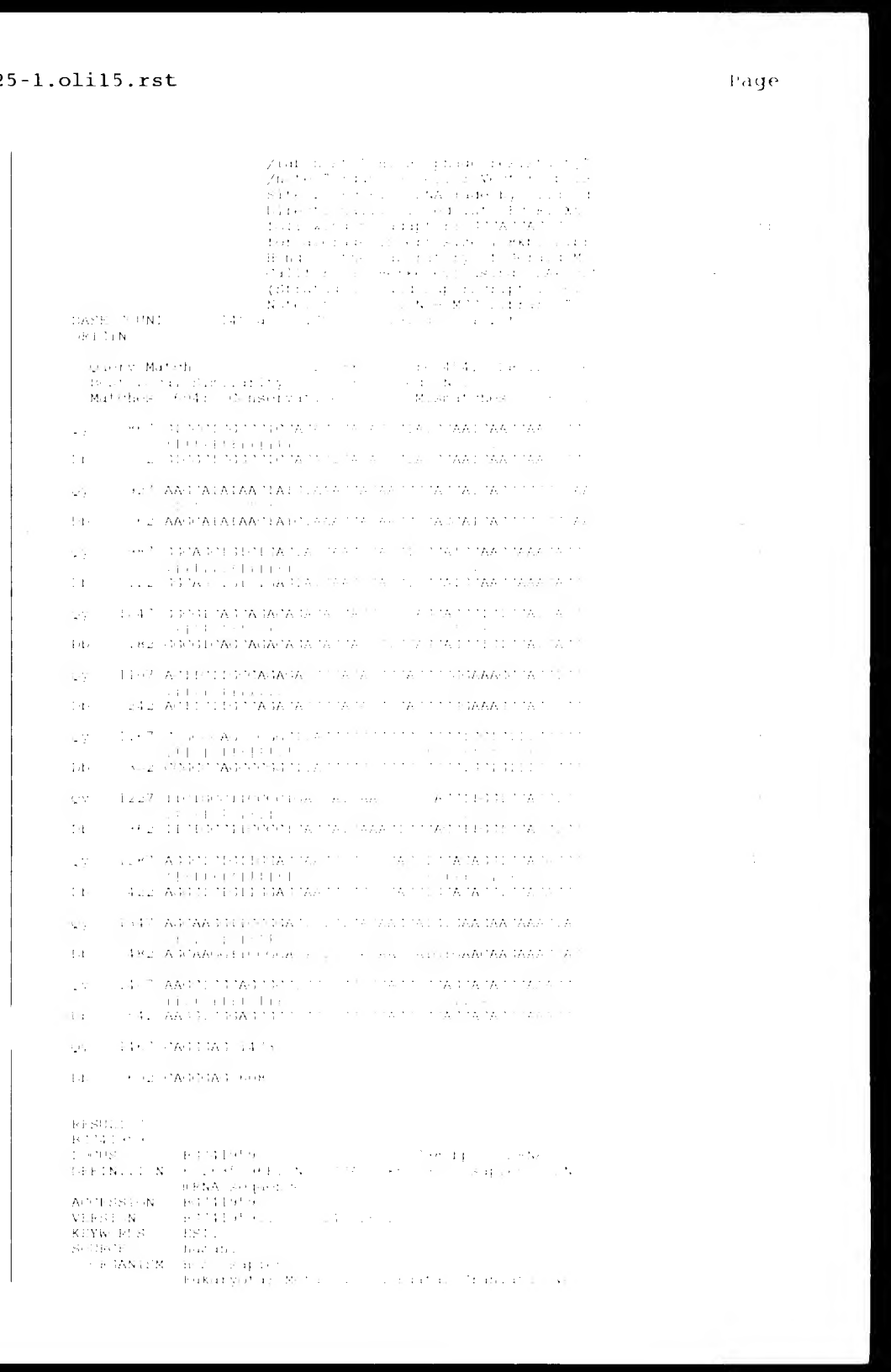

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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: [illegible]
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            cDNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: HAMI96488  row: p  column: 24
            High quality sequence start: 5
            High quality sequence stop: 796.
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                     /db_xref="taxon:9606"
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                     /clone_lib="NCI_CGAP_Skn4"
                     /lab_host="DH10B (T1 phage resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: Sall; Cesgen non-directional; 1.7kb; Size
                     Average insert size 1.5kb; Library constructed by
                     Jeffrey Trent; Note this is a NCI CGAP Library"
BASE COUNT      [illegible]
ORIGIN

  Query Match             [illegible]  Score 436;  DB 12;  Length [illegible];
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  [illegible];  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

RESULT 2
BG486404
LOCUS       BG486404                 588 bp    mRNA    linear   EST 11-MAY-2001
DEFINITION  [illegible] NIH MGC_48 Homo sapiens cDNA clone IMAGE:4796295 5',
            mRNA sequence.
ACCESSION   BG486404
VERSION     BG486404.1  GI:13417701
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   [illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Lind Staudt/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            cDNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: HUMH62S  row: a  column: 04
            High quality sequence stop: 582.
FEATURES             Location/Qualifiers
     source          1..588
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4766019"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B cells from tonsil + (cell line)"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: B cells; Vector: pcDNA7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT primed,
                     directionally cloned into EcoRI/XhoI sites; Site 2
                     following 5' adaptor: GGACGAG(G). Size selected >500bp
                     for average insert size 1.8kb. Library constructed by Lind
                     Staudt in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP cDNA synthesis kit
                     (Stratagene); and Superscript II RT (Life Technologies)
                     Note: this is a NIH_MGC Library."
BASE COUNT      136 a    123 c    178 g    101 t
ORIGIN

  Query Match             21.9%;  Score 427;  DB 12;  Length 588;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  527;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]
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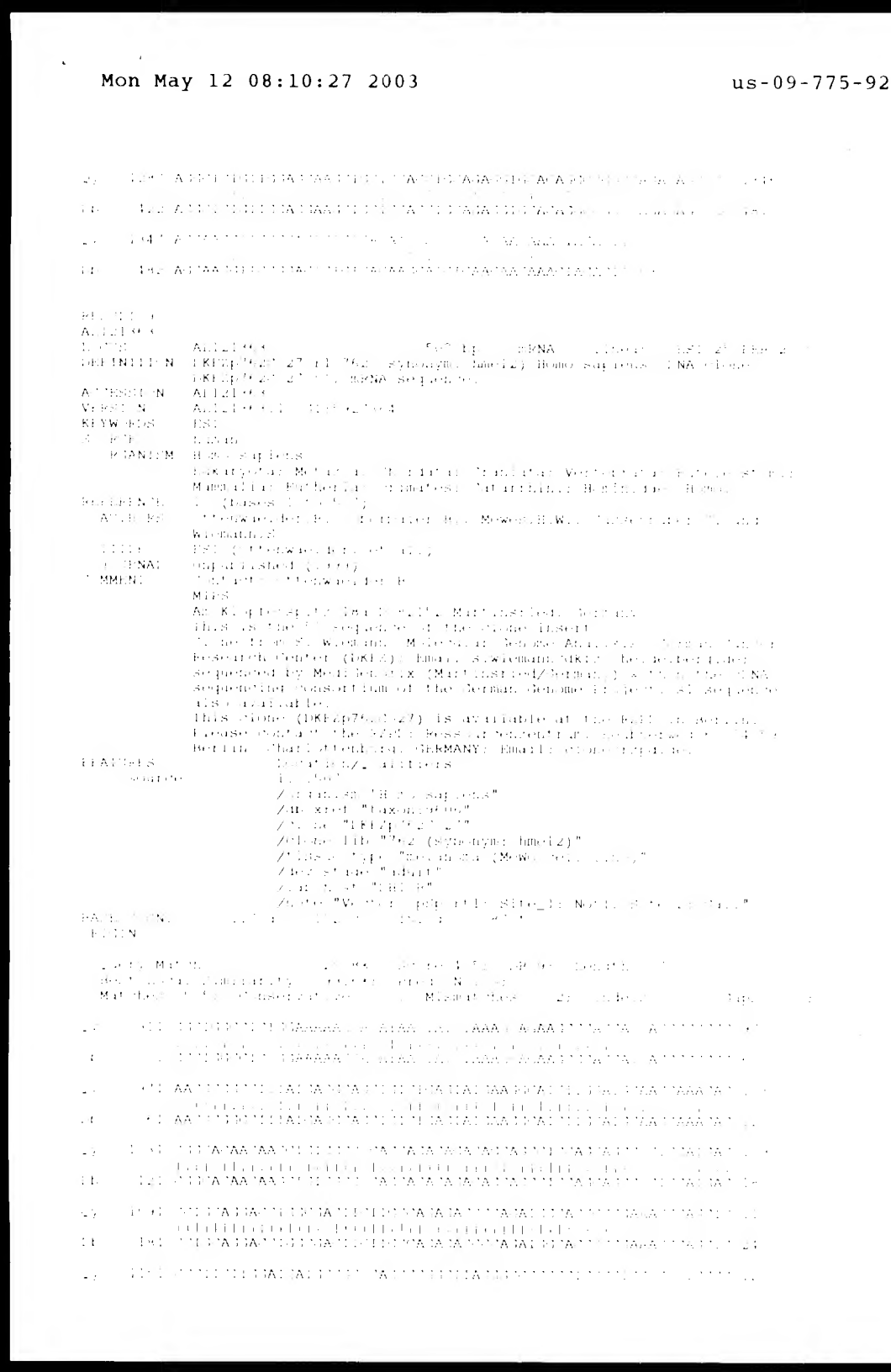

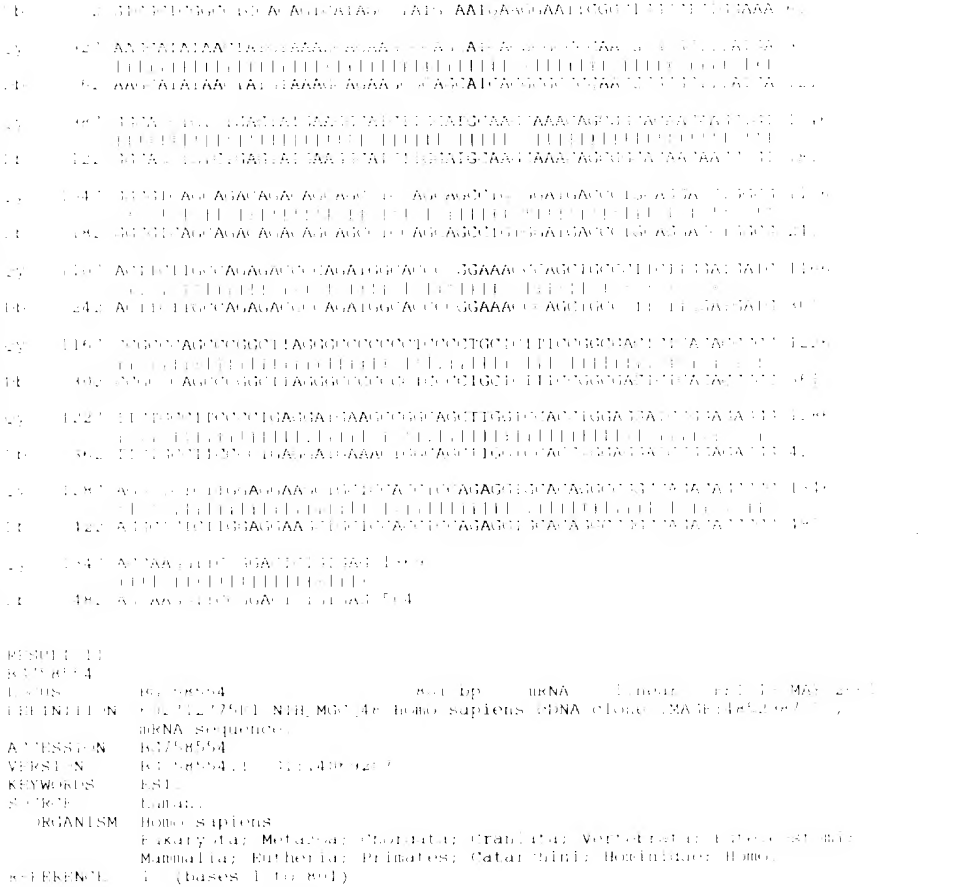

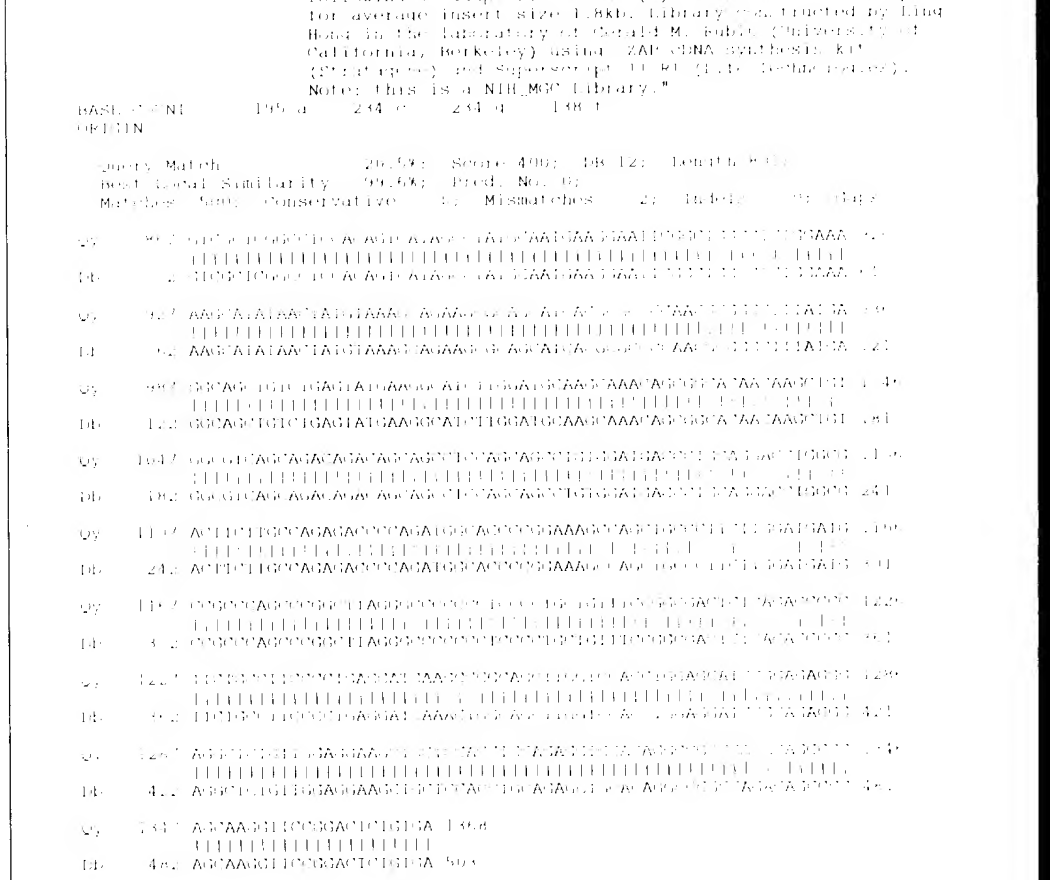

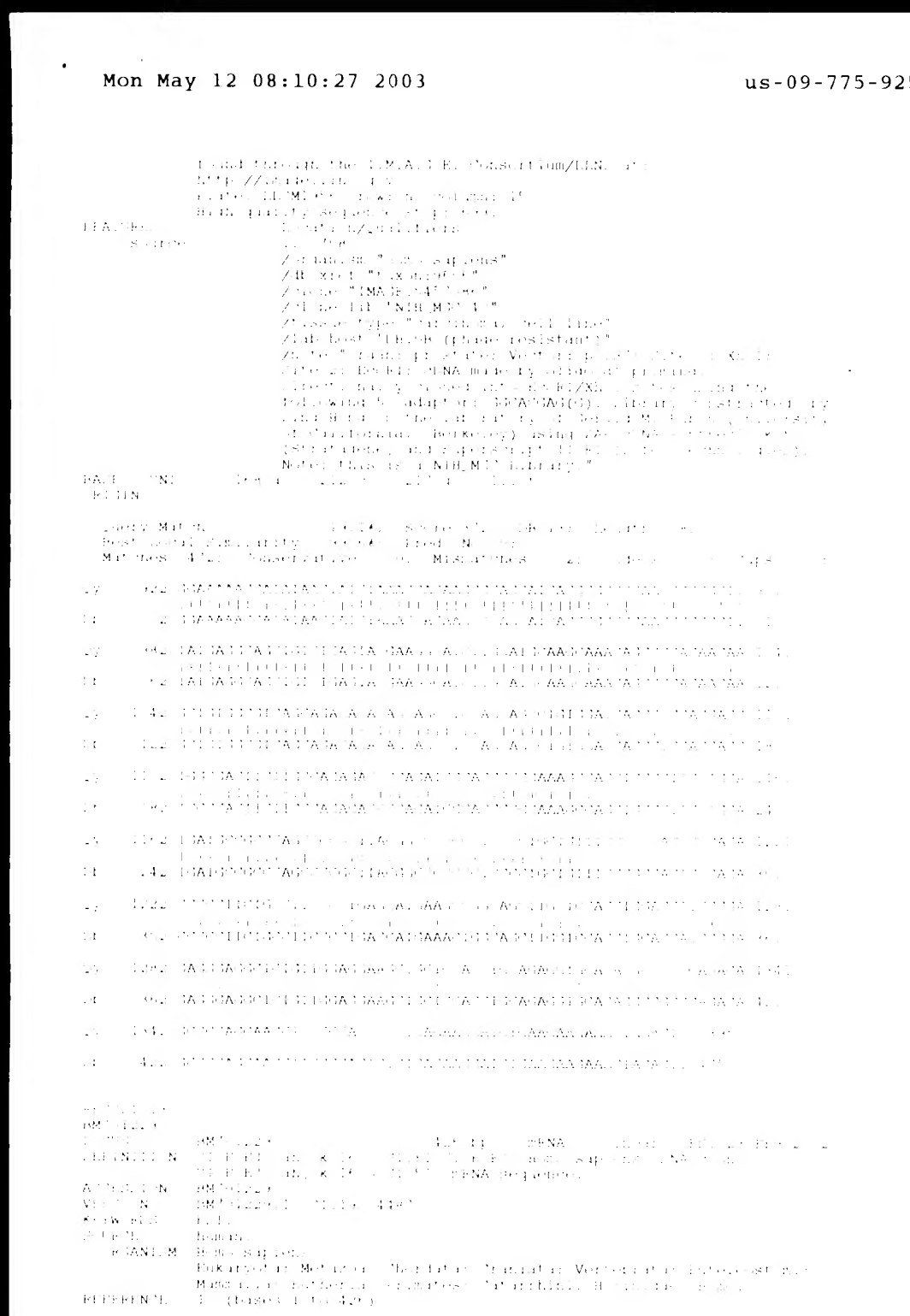

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Qy   1427 [illegible] 1486
Db    [illegible]

Qy   1487 [illegible]
Db    [illegible]

Qy   1547 A[illegible] 1552
Db    4[illegible] A[illegible] 426


RESULT 14
BG397630
LOCUS       BG397630                 954 bp    mRNA    linear   EST 12-MAR-200[illegible]
DEFINITION  [illegible] NIH_MGC_48 Homo sapiens cDNA clone IMAGE:[illegible]
            mRNA sequence.
ACCESSION   BG397630
VERSION     BG397630.1  GI:13291678
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 954)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1281  row: e  column: 1[illegible]
            High quality sequence stop: 792.
FEATURES             Location/Qualifiers
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                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:4564986"
                     /clone_lib "NIH_MGC_48"
                     /tissue_type "primary B-cells from tonsils (cell line)"
                     /lab_host "DH10B (phage-resistant)"
                     /note "Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected on 1%
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and SuperScript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT    [illegible] a    276 c    2[illegible] g    154 t    2 others
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB 12;  Length 954;
  Best Local Similarity   99.[illegible]%;  Pred. No. 0;
  Matches [illegible];  Conservative  0;  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy    [illegible] AAATGAA[illegible]
Db      2 [illegible]

Qy    [illegible]
Db    [illegible]

Qy   1067 [illegible] 1126
Db    [illegible]

Qy   1127 [illegible] 1186
Db    [illegible]

Qy   1187 [illegible]
Db    [illegible]

Qy   1167 [illegible] 1226
Db    362 [illegible] 421

Qy   1227 [illegible] 1286
Db    362 [illegible] 421

Qy   1287 [illegible] 1346
Db    422 [illegible] 481

Qy   1347 [illegible] 1406
Db    [illegible]

Qy   1407 [illegible] 1466
Db    [illegible]

Qy   1467 CAGGGAGGTGGGGCAGCTTCAACT 1492
          ||||||||||||||||||||||||
Db    [illegible] 627


RESULT 15
BM908891
LOCUS       BM908891                 1134 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6611661 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:[illegible]
            5', mRNA sequence.
ACCESSION   BM908891
VERSION     BM908891.1  GI:1935927[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1134)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1903  row: n  column: 08
            High quality sequence stop: 5[illegible]3.
FEATURES             Location/Qualifiers
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                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:5431495"
                     /clone_lib "NIH_MGC_98"
                     /tissue_type "astrocytoma grade IV, cell line"
                     /lab_host "DH10B (phage-resistant)"
                     /note "Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
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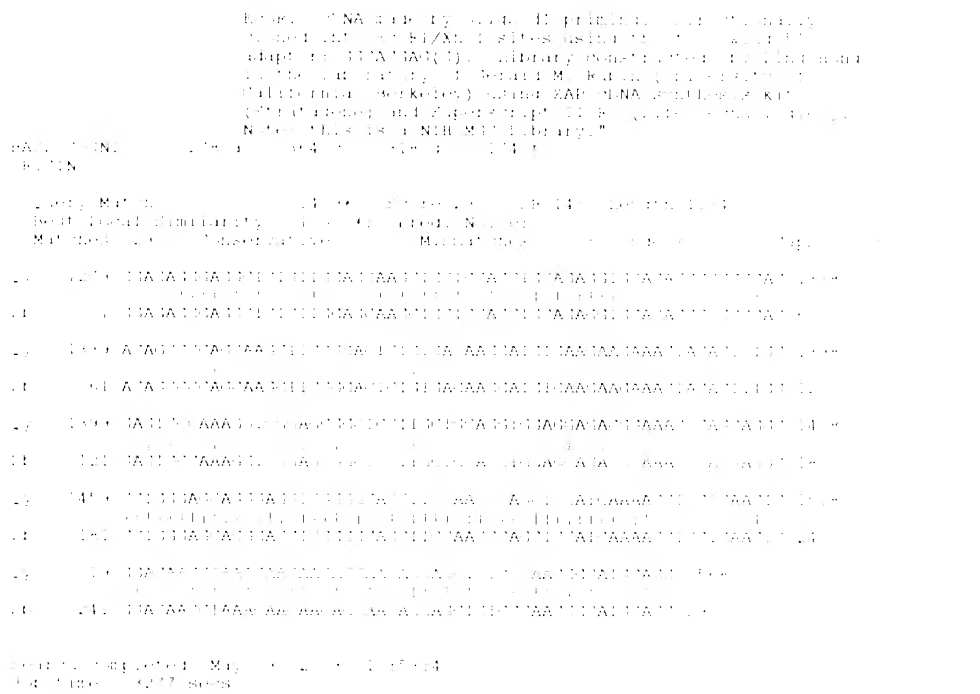
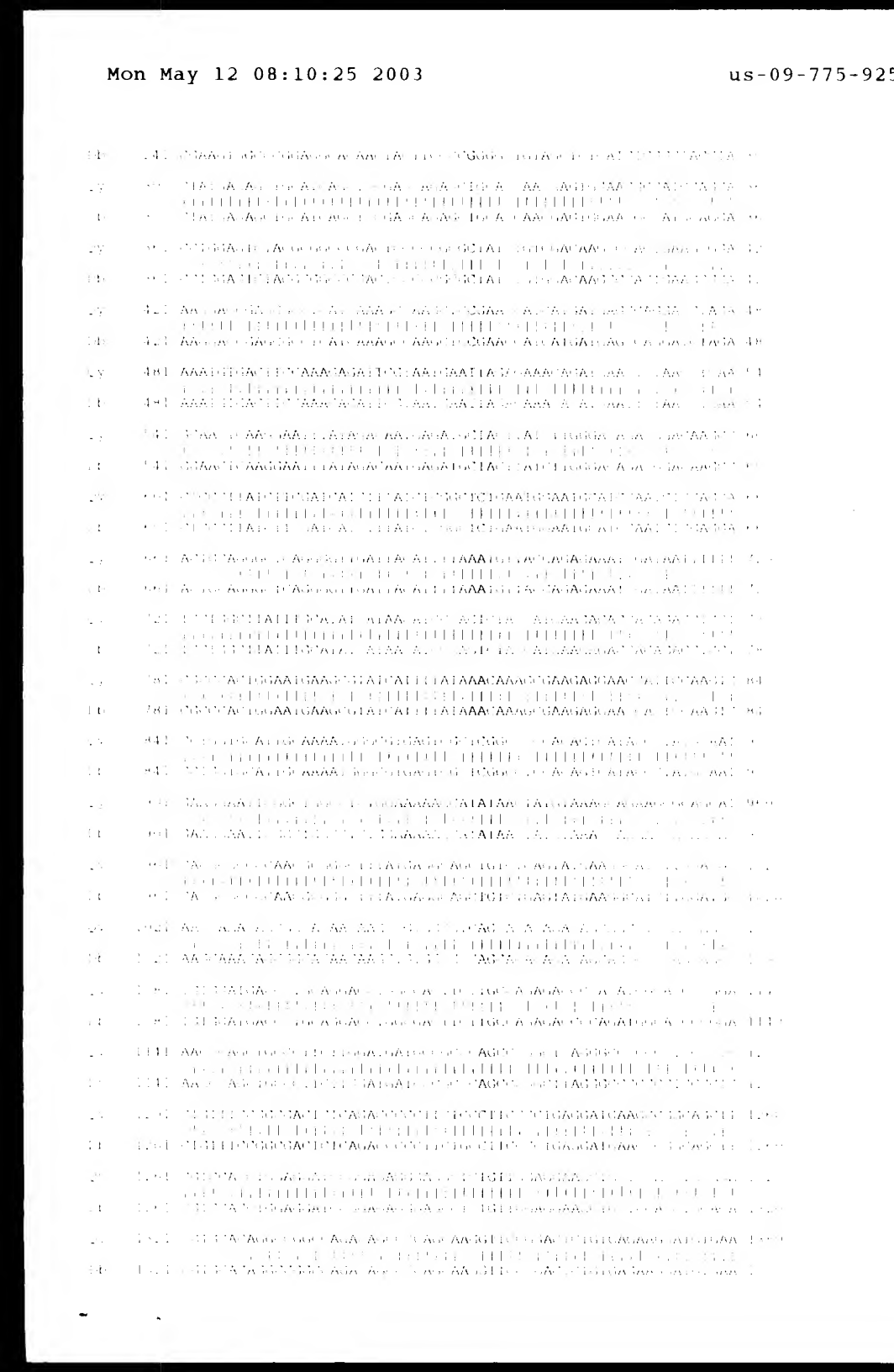
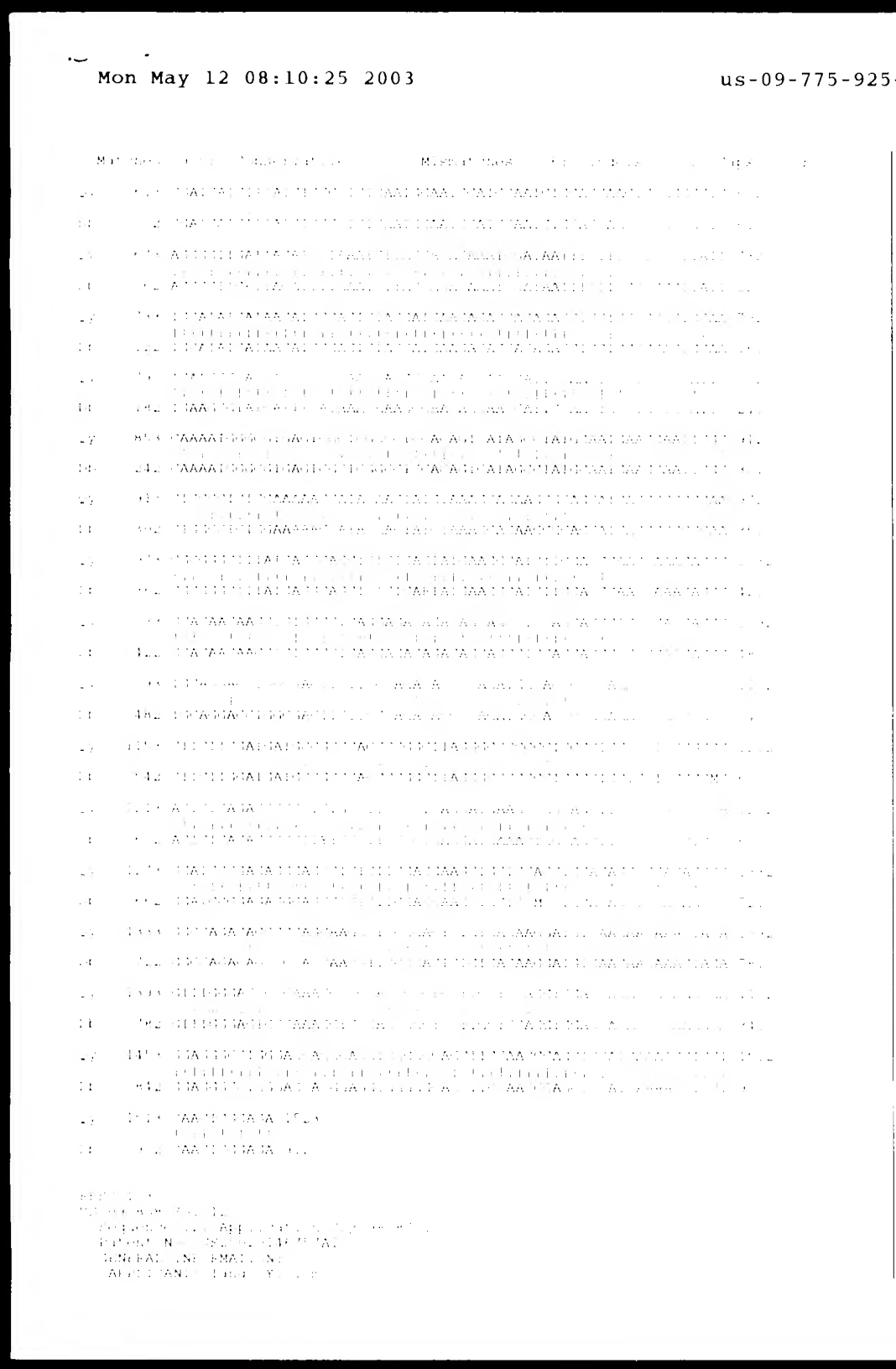




RESULT 2
DS [illegible] 913:78
; [illegible]
; Publication No. US20030008276A1
; GENERAL INFORMATION:
; APPLICANT: Bosch et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ0761
; [illegible]
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 958
; Prior Application removed - See File Wrapper or Docs
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1393)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1445)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1447)
; OTHER INFORMATION: n equals a,t,g, or c
DS 1- [illegible] 913:78

Query Match [illegible] 91.0%; Score 669; DB 9; Length 1450;
Best Local Similarity [illegible]; Pred. No. 6.1e-[illegible];



; TITLE OF INVENTION: Human Genes, Sequences and Expression Products ...
; FILE REFERENCE: PP 16,201
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US/60/179,831
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: misc_feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
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; LOCATION: (418)
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; LOCATION: (446)
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; LOCATION: (472)
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; LOCATION: (476)
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590-1252

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Db 1 ATCTGCGATCAAGAGACAGATCATGAAGTTGGAATGGAAGATTCAGATAGTTATAAA 60

Qy 61 ATAAAAGA 68
||||||||
Db 61 ATAAAAGA 68

RESULT 7
US/09/775,925/1/pe
; Sequence 12, Application US/09/775,925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
; APPLICANT: Lueber, Kali M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: 5/1 12 AND 05 15 TOTAL SEQUENCES
; TITLE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 20012542D
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
RESULT 7
US/09/775,925/12

Score: Match 34.4%; Score 35; DB 11; Length 35;
Best Local Similarity 100.00%; Pred. No. 7e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 645 TTCGATCATCTTATCTCGGCTCTGAATGGAATGC 679
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Db 35 TTCGATCATCTTATCTCGGCTCTGAATGGAATGC 1

RESULT 8
US/09/764,972/576
; Sequence 576, Application US/09/764,972
; Publication No. US20030082761A1

; NUMBER OF SEQ ID NOS: 986
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 969
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-775-925-969

Query Match 1.6%; Score 42; DB 10; Length 1854;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1649 GGGACTACAGGCACCCCCACCACACCACCT 1690
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Db 1276 GGGACTACAGGCACCCCCACCACACCACCT 1317

RESULT 12
US-09-780-669-969/c
; Sequence 969, Application US/09/780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianzhou
; APPLICANT: Dillon, Davin C
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqin
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Rotter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Bepler, William
; APPLICANT: Burat, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Boughton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 21012.427C4
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 969
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: Homo Sapien

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RN   [2]
RP   1-1862
RA   Alderton G.;
RT   "Novel phosphatase polypeptides useful for treating immune";
RL   Submitted (07-NOV-2000) to the EMBL/GenBank/DDBJ databases.
RL   Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850, USA.
XX
RN   [3]
RP   1-1862
RA   Ruben S.M., Rosen C.A., Baughn M.R., Whitmore S.A., Moore P.A., Ebner R.,
RA   Ferrie R.M.;
RT   "Novel phosphatase polypeptides useful for treating immune";
RL   Patent number WO200077044-A/1, 21-DEC-2000;
RL   Human Genome Sciences, Inc. (HUMA-N) Human Genome Sciences Inc. (HUMA-N).
XX
DR   WPI; 2001-104744/11.
DR   N-PSDB; ABL57466.
XX
PT   Novel phosphatase polypeptide, useful for treating immune related diseases and disorders, cardiovascular disease, brain or neuronal associated diseases and metabolic disorders -
XX
PS   Claim 7; Fig 2; 186pp; English.
XX
CC   The present invention relates to phosphatase polypeptides, and the
CC   sequences encoding them, as well as various products and methods useful
CC   for the diagnosis and treatment of various phosphatase related diseases
CC   and conditions. Substance that modulates the activity of phosphatase
CC   polypeptide is used to treat immune-related diseases and disorders,
CC   cardiovascular disease, brain or neuronal associated diseases and
CC   metabolic disorders, including cancers of tissues, cancers of
CC   hematopoietic origin, diseases of central and peripheral nervous
CC   system, Alzheimer's disease, Parkinson's disease, multiple sclerosis,
CC   amyotrophic lateral sclerosis, viral infections, infectious mononucleosis,
CC   pregnancy, bacteria and fungi, ocular diseases, diabetes, kidney disease,
CC   sexual dysfunction, mood disorders, affective disorders, cognitive
CC   disorders, hypotension, hypertension, psychotic disorders, neurological
CC   disorders, dyskinesias and organ transplant rejection. The present
CC   novel human phosphatase polypeptide sequence is human SH2-containing
CC   phosphatase polypeptide. The sequence is classified as dual specificity phosphatase (DSP) and MAP
CC   kinase phosphatase (MKP). SHPTP2 gene maps to chromosome position
CC   12p12.3-p13.
XX
SQ   Sequence  1862 AA;

  Query Match             88.9%;  Score 1411;  DB 23;  Length 1944;
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  Matches  441;  Conservatives   11;  Mismatches   30;  Indels    5;  Gaps    1;

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Db       41 MVTSRWRRPEPRPIPVPSPAFSMDNLQTQERWRSLQRVEVSDFDSIQDLKAQLVETAGLHPE  100

Qy       61 IVALWAIYELSKNNPQDLLDVKPDGKFEHDNGKNLRLFVAECPEPVLTQIELNTISYPDHL  120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      101 IVALWAIYELSKNNPQDLLDVKPDGKFEHDNGKNLRLFVAECPEPVLTQIELNTISYPDHL  160

Qy      121 TSRNFPDKNIEFIHSHLKAEDTDTVIHCSAGAGRTGTFIVIDAMLDMMHSERKVDVYGFVS  180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 TSRNFPDKNIEFIHSHLKAEDTDTVIHCSAGAGRTGTFIVIDAMLDMMHSERKVDVYGFVS  220

Qy      181 RIRAQRCQMVQTEAQYVFIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE  240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      221 RIRAQRCQMVQTEAQYVFIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE  280

Qy      241 FQWLPHFSKLSDRHNESNESGDESDQALFLTEPGSPRSAPHGPWGAKQLNSTLSLITAVGD  300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      281 FQWLPHFSKLSDRHNESNESGDESDQALFLTEPGSPRSAPHGPWGAKQLNSTLSLITAVGD  340

Qy      301 SQQRDDSSSPNATVNQKRARLRPQGQLWRASEAPNSLDALMQCFYLQKCPMNMPTQLSRAY  360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      341 SQQRDDSSSPNATVNQKRARLRPQGQLWRASEAPNSLDALMQCFYLQKCPMNMPTQLSRAY  400

Qy      361 EVPLDPSVMFPRRLSHRLPDNSGHIFPFPETQSIVVESVELEDPEWAAIFHNAQPKAREGH  420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      401 EVPLDPSVMFPRRLSHRLPDNSGHIFPFPETQSIVVESVELEDPEWAAIFHNAQPKAREGH  460

Qy      421 LDKQPESPVRKKLEPPSPKCRSVDSIESGFSSEGFSLDYTQRVCAGLPCKCKSRMVSGQCL  480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      461 LDKQPESPVRKKLEPPSPKCRSVDSIESGFSSEGFSLDYTQRVCAGLPCKCKSRMVSGQCL  520

Qy      481 SEGSSDYCNSSTLPSEYKKAYPAPEAFARSPSVRSEKRVSSMNNSMVSIDAKVMSWEDSK  540
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Db      521 SEGSSDYCNSSTLPSEYKKAYPAPEAFARSPSVRSEKRVSSMNNSMVSIDAKVMSWEDSK  580

Qy      541 SKSQNADVVCLISVTDLEKQDEFLWSHRHYLESKSDQGSEFMQSFGRIDQEKSEDAYDVLR  600
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Db      581 SKSQNADVVCLISVTDLEKQDEFLWSHRHYLESKSDQGSEFMQSFGRIDQEKSEDAYDVLR  640

Qy      601 DQRQEEVNNSHSTGNQWKNENNPLYGNPQFTSTAVVPNIAEKMQSDIPPHLLTPVGESLPH  660
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Qy      661 PPGFTLSTSSVTSLHSSPISSNSPLSSSNAAEIQMQTAVAIHIGDSIPGLEASEASHLSSE  720
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Db      701 PPGFTLSTSSVTSLHSSPISSNSPLSSSNAAEIQMQTAVAIHIGDSIPGLEASEASHLSSE  760

Qy      721 EKDSLYADLDFVAGASGNGTSSTSGGLEMYAQVSKPSPNREVVDEMPHSRIPENLENPEER  780
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Qy      781 PERIQELKGQISDKDFESGKYGFRSNYKDVYNKTVLPYDHNRVELSLINEDDESDYINANF  840
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      881 IKGVNEPREFIATQGPLPNTVNDFWRMIWEQKSATIVMMVTRCEEGNRNKCAEYWPSMEEG  940

Qy      901 TRAFGDVVVKINQHKRCPDYIIQKLNIVNKKEKATGREVTHIQFTSWPDHGVPEDPHLLLK  960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      941 TRAFGDVVVKINQHKRCPDYIIQKLNIVNKKEKATGREVTHIQFTSWPDHGVPEDPHLLLK  1000

Qy      961 LRRRVNAFSNFFSGPIVVHCSAGVGRTGTFIGIDAMLEGLEAENKVDVYGYVVKLRRQRCL  1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1001 LRRRVNAFSNFFSGPIVVHCSAGVGRTGTFIGIDAMLEGLEAENKVDVYGYVVKLRRQRCL  1060

Qy     1021 MVQVEAQYILIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAEFQRLPSYR  1080
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Qy     1081 SWRTQHIGNQEENKSKNRNSDIIPFDYNRVPLKHELEMSKESEHDSDESSDDPSSPPLIQN  1140
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Qy     1141 FIQRGASCVTHPEVEKTALDNYGMSLDGGYVRENIGSEMHRTRVDSPASSLSSTASWLPE  1200
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Qy     1321 YLTLVDLSAKDVEKIHLIDNSLDFTMRKQKFHFVAQWPDHGVPESVDPILSLIRTVRDYS  1380
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Qy     1381 KQSPGKEKPIVVHCSAGIGRTGTFVVIDSMLDMMHNERKVDVYGHVTCMRSQRNYMVQTE  1440
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Qy     1441 AQYVFIHDTLVEAIKSKETEVPAENIWKQFQSLNIKDFKLSDVTSNWSEERTKLAFFEFP  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     1501 KTLFSIFNLIDKDIHSRWSALEIGILYDCLDTMDQYKVKLAEYEASISEAQEGERKSKVF  1560
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Db     1541 KTLFSIFNLIDKDIHSRWSALEIGILYDCLDTMDQYKVKLAEYEASISEAQEGERKSKVF  1600

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Qy     1741 VSAEHSFPEYLSAVNLGHSNNIVEKLVPRIDEVIKTDAKSKNDPIGITVHDRKDRTQTLK  1800
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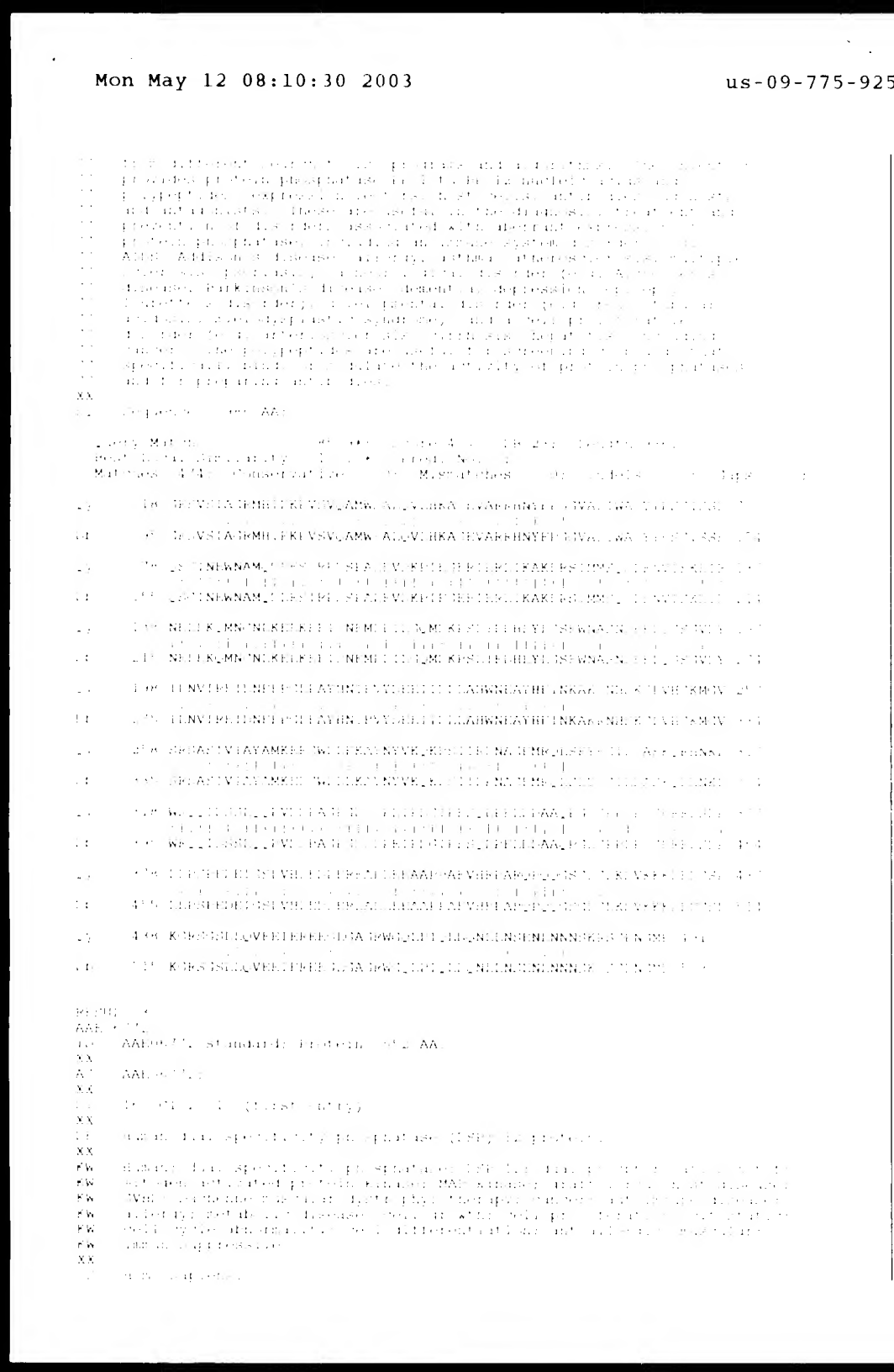

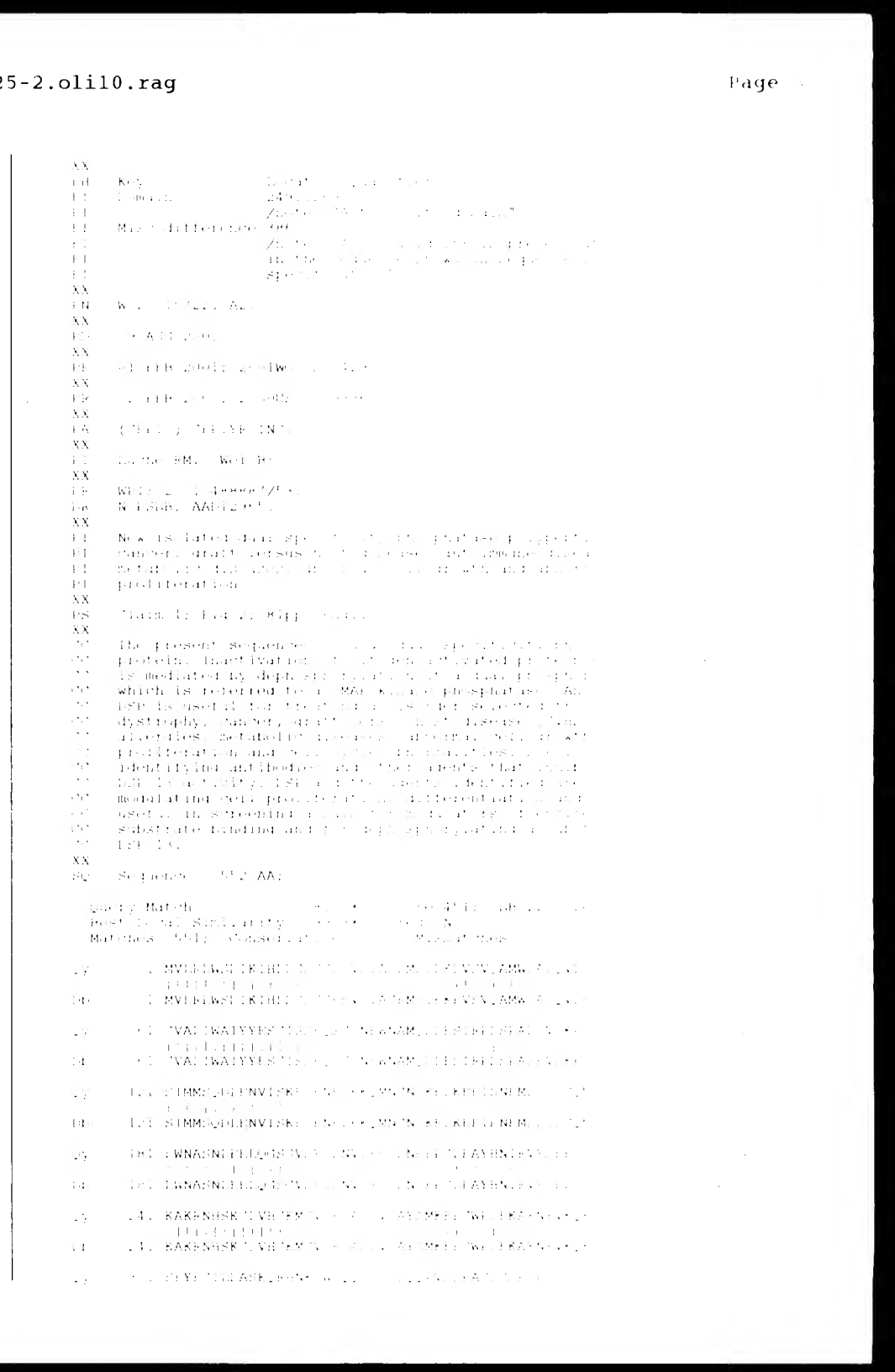

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PR 06 DEC 2000; 2000US-0251671.
PR 06 DEC 2000; 2000US-0251879.
PR 08 DEC 2000; 2000US-0251805.
PR 08 DEC 2000; 2000US-0251868.
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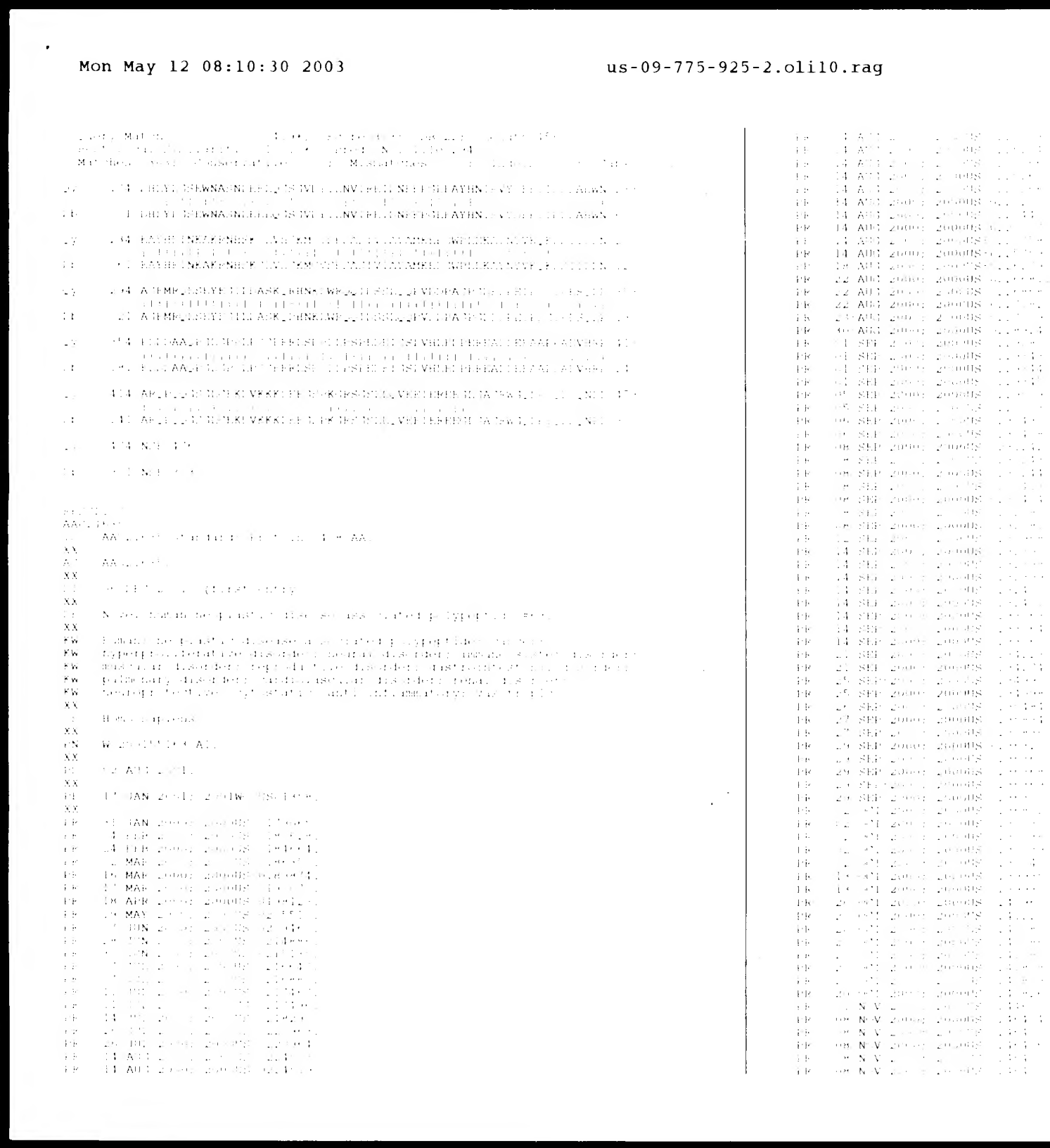
PR 11 DEC 2000; 2000US-0254097.
PR 05 JAN 2001; 2001US-0259078.
XX
PA (HUMA) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
DR N-PSDB; AAS41087.
XX
PT Novel polypeptides and polynucleotides useful for diagnosis,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases
XX
PS Claim 11; SEQ ID No 1514; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS41085 AAS41084, and AAS41086) sequences
CC encoding them. The enzyme polypeptides of the invention are comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC diseases including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
CC blood related disorders (e.g. haemophilia), reproductive disorder
CC (e.g. infertility) and infectious disorders (e.g. tuberculosis). The
CC polynucleotides of the invention can also be used in gene therapy.
CC AAU22615 AAU23614 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 458 AA;



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RL   17 NOV 2000; 2000US-0249265.
RL   17 NOV 2000; 2000US-0249266.
RL   17 NOV 2000; 2000US-0249300.
RL   [illegible] 2000; 2000US-0250[illegible].
RL   [illegible] 2000; 2000US-0250[illegible].
RL   05-DEC-2000; 2000US-0251988.
RL   [illegible] 2000; 2000US-0252[illegible].
RL   06-DEC-2000; 2000US-0251479.
RL   08-DEC-2000; 2000US-0251868.
RL   08-DEC-2000; 2000US-0251869.
RL   08-DEC-2000; 2000US-0251870.
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RL   [illegible] 2000; 2000US-0252[illegible].
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RL   [illegible] 2000; 2000US-0254[illegible].
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RA   [illegible] S.M.MAN-SUN-MUI [illegible].
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RT   "Novel [illegible] Batash 35" Filed: 2M.
XX
RL   WO[illegible]-A2-0[illegible]58/[illegible].
DR   N-PSDB; AAG58064.
XX
CC   Novel polypeptides and polynucleotides used as diagnostic targets
CC   for use in diseases or disorders associated with aberrant expression;
CC   useful for producing polypeptides, and for treating cancers, the AIDS
CC   virus, arthritis
XX
SQ   Sequence 476 AA;

  Query Match             94.9%;  Score 903;  DB 22;  Length 476;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-294;
  Matches  903;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      174 PHLYIGSEWNASNLLLAPSCVEYILNVTRECIDNFFHCGIEAYHNIPVYDLEITGILAHWN 233
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Db        1 PHLYIGSEWNASNLEELAPSCVEYILNVTRECIDNFFHCGIEAYHNIPVYDLEITGILAHWN 60

Qy      234 LAYHILTGKAKENSEEKLYWEIMKVTQEAGKVLAQAMEPLKWTLEEAYNKYVKKDCTPFEN 293
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Db       61 LAYHILTGKAKENSEERLYWEIMKVTQEAGKVLAQAMEPLKWTLEEAYNKYVKKDCTPFEN 120

Qy      294 AQPNEQLSEVEDSLQSAEKQKSNEIWPQQGTDSSLQQPVDDPAGPGDPLPEEIPDTIPESQLP 353
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Db      121 AQPNEQLSEVEDSLQSAEKQKSNEIWPQQGTDSSLQQPVDDPAGPGDPLPEEIPDTIPESQLP 180

Qy      354 FLDDAAQPSILGPPLPCCPRRLSDPLLPSPEDEPGSLVHLLEDPERKALLEEAAPLAEVHRP 413
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Db      181 FLDDAAQPSILGPPLPCCPRRLSDPLLPSPEDEPGSLVHLLEDPERKALLEEAAPLAEVHRP 240

Qy      414 AHQNQQASSLQAEKVKKKIFKIGSPKSSASISQVEEITSPETSGAGHWSQPSLTPLNEI 471
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Db      241 AHQNQQASSLQAEKVKKKIFKIGSPKSSASISQVEEITSPETSGAGHWSQPSLTPLNEI 298

Qy      474 NSE 476
            |||
Db      299 NSE 301


RESULT 4
AAF06785
ID   AAF06785 standard; Protein; 176 AA.
XX
AC   AAF06785;
XX
DT   26-OCT-2000 (first entry)
XX
DE   Human dual specificity phosphatase (DSP) 1z partial protein.
XX
KW   Human; dual-specificity phosphatase; DSP 1z; dual phosphorylation activity;
KW   stress-activated protein kinase; MAP-kinase; graft versus host disease;
KW   SVIBG; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease;
KW   allergy; metabolic disease; cell growth; cell proliferation; cytostatic;
KW   cell cycle abnormality; cell differentiation; antiviral; muscular;
KW   immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   WO200157221-A2.
XX
PD   09-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04111.
XX
PR   08-FEB-2000; 2000US-0179886.
XX
PA   (CEFT ) CEPTYR INC.
XX
PI   Lange RM, Wei B;
XX
DR   WPI; 2001-438897/54.
XX
PT   New isolated dual specificity phosphatase polypeptide for treating
PT   cancer, graft-versus host disease, autoimmune diseases, allergies,
PT   metabolic diseases, abnormal cell growth and abnormal cell
PT   proliferation
XX
PS   Example 1; Fig 6; 80pp; English.
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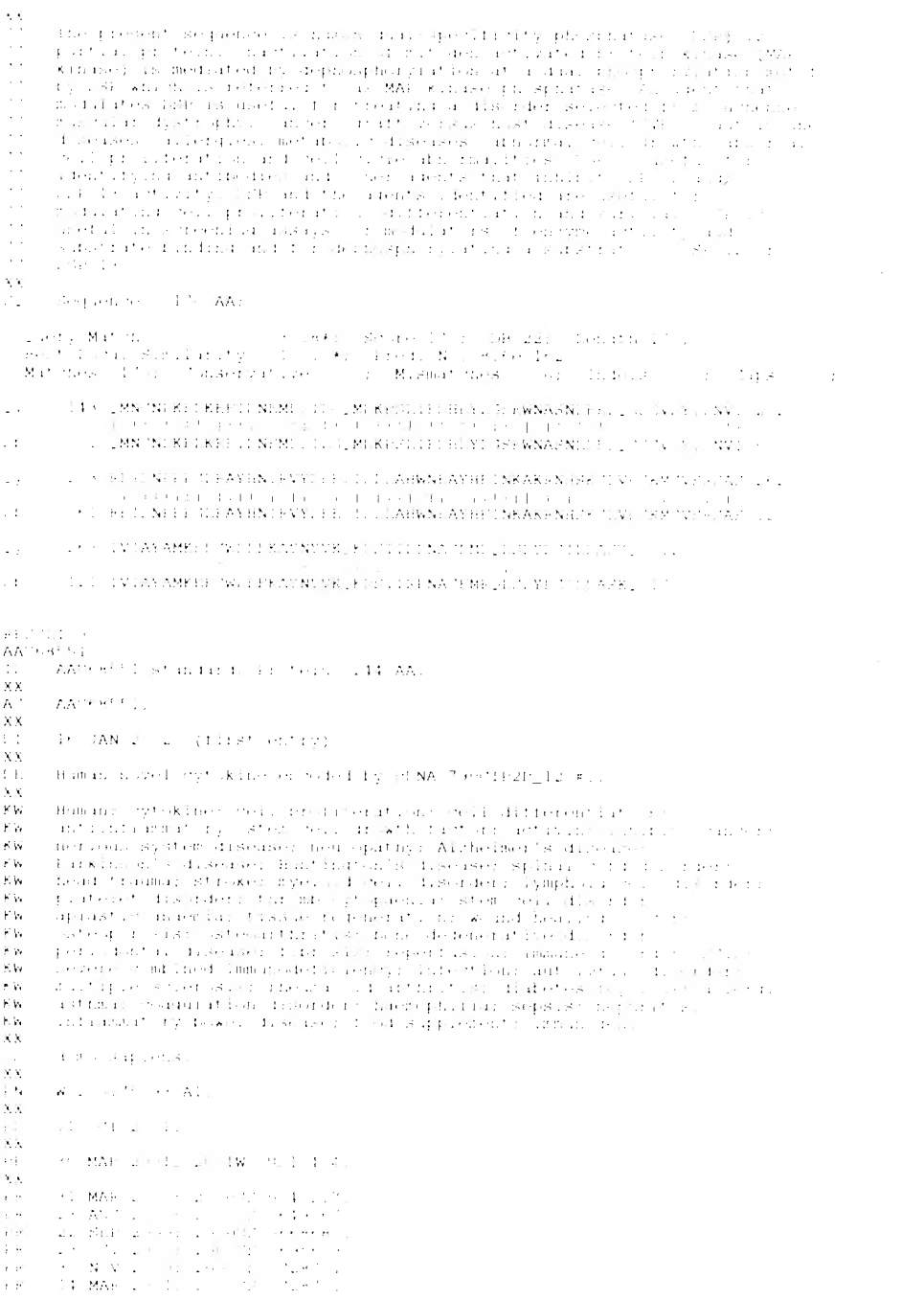

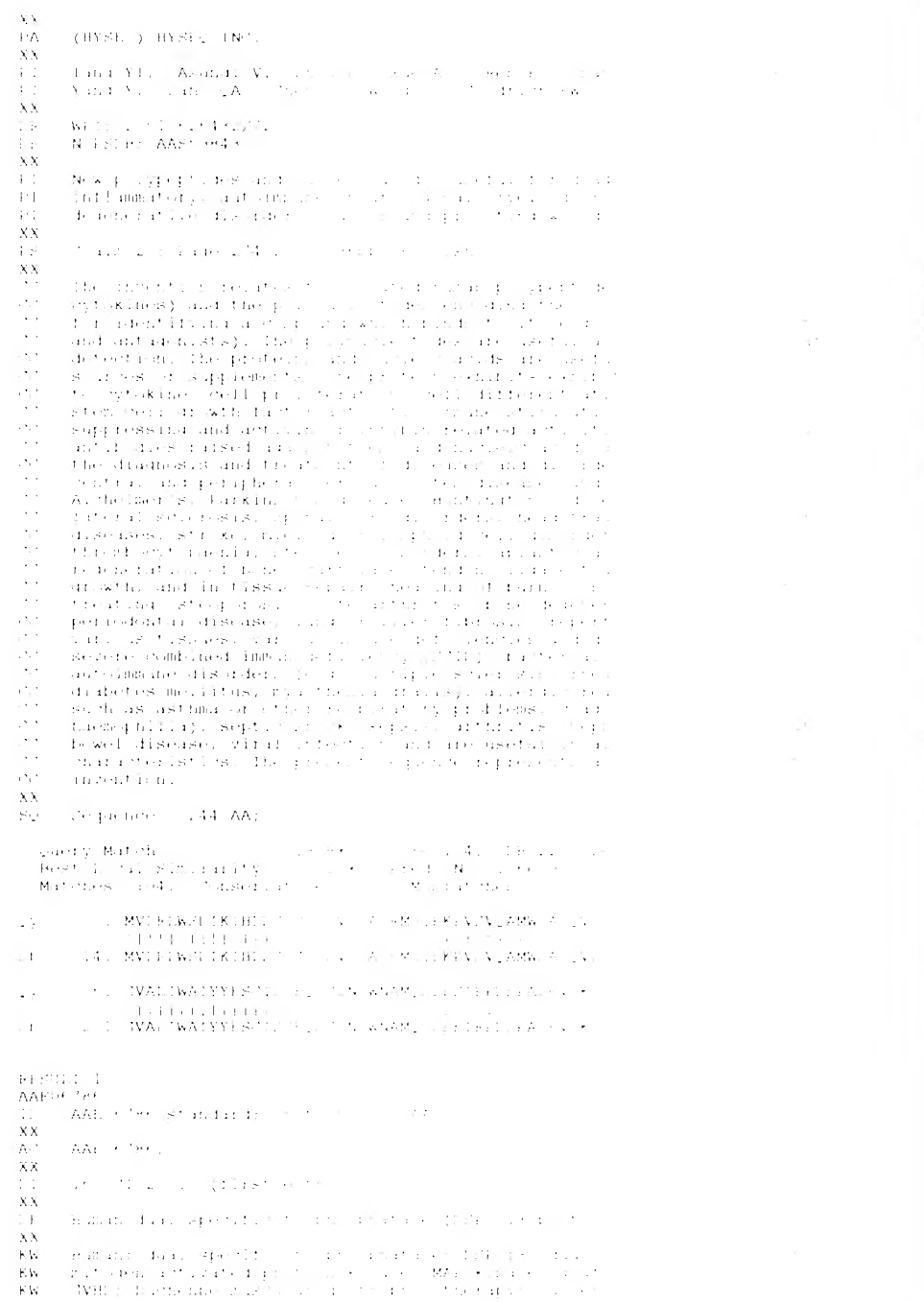

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KW    diabetes; metabolic disease; cell growth; cell proliferation; cytostatic;
KW    cell cycle abnormality; cell differentiation; autoimmune disease;
KW    immunosuppressive.
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  Query Match             4.5%;  Score 25;  DB 22;  Length 241;
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Qy     127 SKCVHCKMCVSKSASIVIAYAMKE 151
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Db     127 SKCVHCKMCVSKSASIVIAYAMKE 151


RESULT 2
AAE22738
ID   AAE22738 standard; protein; 417 AA.
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AC   AAE22738;
XX
DT   09-AUG-2002  (first entry)
XX
DE   MAP kinase phosphatase consensus protein Sequence #2.
XX
KW   dual specificity phosphatase 1; DSP-1; antihistaminic; hypotensive;
KW   immunosuppressive; MAP; mitogen activated protein kinase; cancer; enzyme;
KW   signal transduction; cell proliferation; Duchenne muscular dystrophy;
KW   cell cycle abnormality; graft versus host disease; autoimmune disease;
KW   metabolic disease; allergy; screening.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FH   Misc-difference 16
FT                   /note= "Represented as the specific amino acid."
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PN W2003/032121 A2.

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PD 03-APR-2003.

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PF 02-OCT-2002; 2002WO-US031420.

XX

PR 02-OCT-2001; 2001US-0326420P.

XX

PA (SCRI) SCRIPPS RESEARCH INST.

XX

PI Fischer EH, Wei B.

XX

DR WPI; 2003-388787/36.

DR N-PSDB; AAU12955.

XX

PT Novel isolated dual specificity phosphatase polypeptide for treating cancer, graft versus host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth and abnormal cell proliferation

XX

PS Claim 56; Fig 4; 81pp; English.

XX

CC The present sequence is human dual specificity phosphatase (DSP) 1. The protein, inactivation of mitogen-activated protein kinase (MAP kinase) is mediated by dephosphorylation at a dual phosphorylation motif by DSP, which is referred to as MAP kinase phosphatase. An agent that modulates DSP is useful for treating a disorder selected from leukemia, muscular dystrophy, cancer, graft versus host disease (GVHD), autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation, and cell cycle abnormalities. DSP is used in identifying antibodies and other agents that inhibit DSP activity. DSP and the agents identified are used in modulating cell proliferation, differentiation and survival. DSP is useful in screening assays for activators and enzymes, and substrate binding and for dephosphorylating a substrate of DSP 1

XX

SQ Sequence 509 AA;

Query Match 4.0%; Score 25; DB 22; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.5e+16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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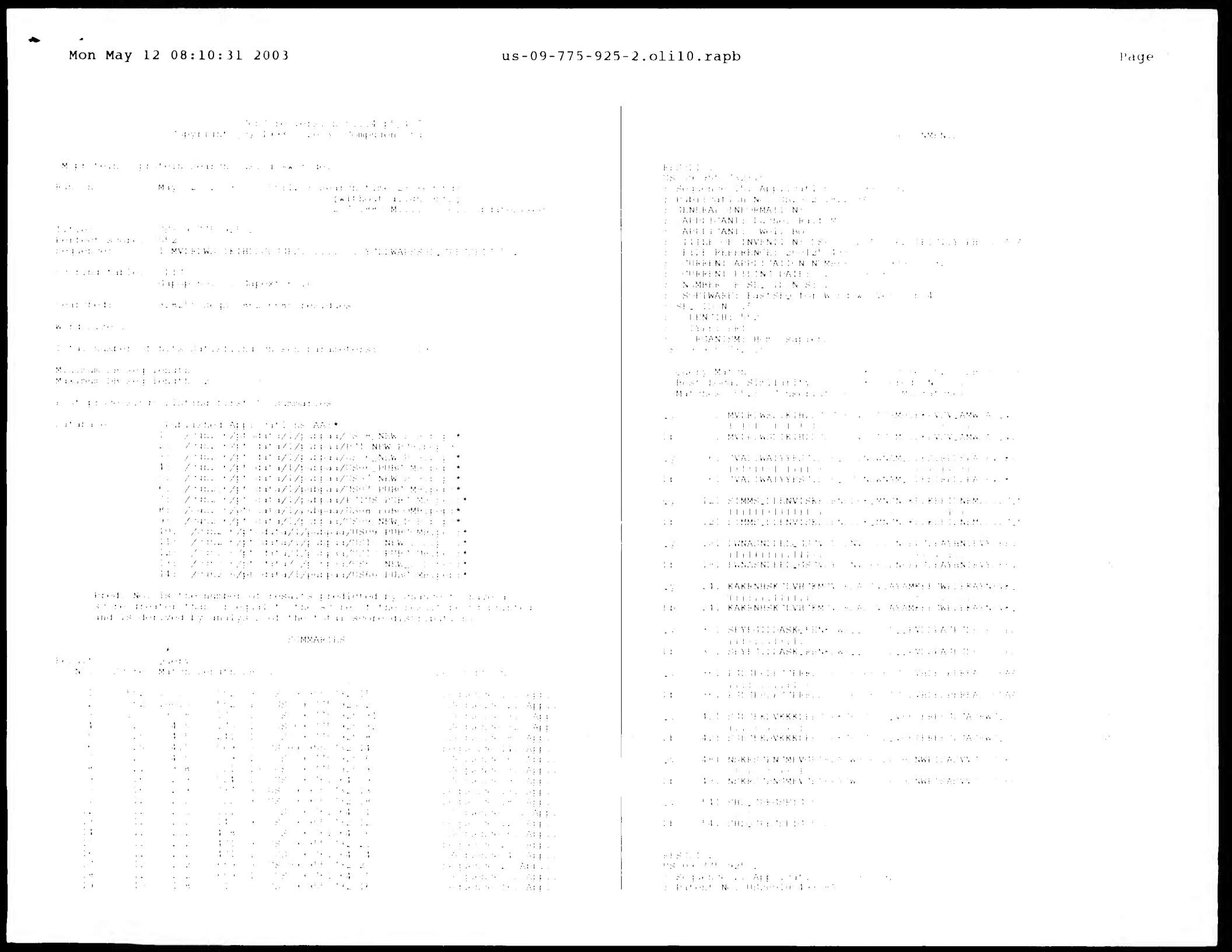

; GENERAL INFORMATION:
; APPLICANT: Luche, Rolf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP 1.2 AND DSP 1.3 DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-2

Query Match 100.0%; Score 552; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSVLAPPAAPGFRVAVASATDVELTWDDNSIEDESGFVIERKIAGENSWAQIGQVGANVTSYSVTGLTPGVEYDFRVFAYNDAGDSLPLVAQATTKMAPAPTDVTATAVSPTSIDLTWKAPDKDFDHYRIEKSSDGVTYVEVGEVLTYSDTGLAPNTEYHYRVVAVNGAGESPPSEASATTLPVPGSSYNLTFDITGLKMGGITYLWEGTPRQNLTLHDCVTKFKIDLPSREHELCFSVEAHNDKGVVTSKPAKETFTPVEPSTLEPNLVLMDVRVTDVTLSWQDPEDPFDSFLIQYQESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVIRGYRTPVLSAEFTTGIDAPRDLTFVQVTDTSITLRWTPPAGNVDSYDVTYSSPEGPKEVVTLPETATSVTLSGLTPGVEYNISLYTMKDDQESVPISDTVIPEVPQLTDLSFVDITDSSIGLRWTPLNSSTIIGYRITVVAAGEGIPIFEDFVDSSVGYYTVTGLEPDTEYDVKVYALNGAGESPASSVKVRTAMAPDQVIDLTATPGSQTSLSLSWTAPVGAVDRYRVDVIPINLPSEHNQLSLLPGRQSEFVVSGLTPGVEYVFYIISEDTVNIHSQPLIAQQTSVIDVPKPLDLTFVEVTDTSLTIRWTPPEAQITGYRLTVGLTRRGQPRQYNVGPSVSKYPLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPVKSLIFKNIRETSVELEWNAPDNKSSQDTLEIEYDISQGGERTERLQEVTSKHVKITGLLPGTTYLFRMRAVNEYGIGDWSEESEVITTPEGVPSAPPDFRAEPGDGQVLLKWKPPLSPNGIITQYIIYWGLVAEEMTQCHVHHRGFVTLRGLRGSTVYTLTVLAFTSVGDGPLSSRAIRTQSEELLDQMPSDFKIEDLGSDYVRLSWNYFDSEAIQGFLIVYAPVNKSMDRRFAEPGRQSTEFTVPGLEEFTPYSFYMVAFTEAGDGIQSLEPVKQSTTLAAVIGCMAVVVLAVLCLVAIMYVFCCKNDSSKLDYRDDDAAQTANGNSRETSYIDPDMYVPPDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTVQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSSVLYTAVQPNEGDNDYIIPLPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAEDSFL

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-31

Query Match 90.8%; Score 125; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPCNLKEIKEPTENLMELTGQMSKIGTFEMEYTQSEWNASNEELQVSVETLNVT 57
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Db 1 MSPCNLKEIKEPTENLMELTGQMSKIGTFEMEYTQSEWNASNEELQVSVETLNVT 57

Qy 58 IKLFHNGDQALTLYVSQTTQTAGIYNLTIHGDKFATETITIKVVDKAFVEPHLRMLG 114
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 58 IKLFHNGDQALTLYVSQTTQTAGIYNLTIHGDKFATETITIKVVDKAFVEPHLRMLG 114

Qy 115 NKGQNSIGFKVKPLSEFVKKLEEGSKGKISSLQREIELVEEEREGLQKSWKQLPLSN 171
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Db 115 NKGQNSIGFKVKPLSEFVKKLEEGSKGKISSLQREIELVEEEREGLQKSWKQLPLSN 171

Qy 172 SKQLVHQKMQVSRQASIVIAYAMKELAQMELTSKVAVVSVSTQPKSIDKSDGSLDSK 228
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 172 SKQLVHQKMQVSRQASIVIAYAMKELAQMELTSKVAVVSVSTQPKSIDKSDGSLDSK 228

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-32

Query Match 4.5%; Score 25; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.8e-1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 SKQLVHQKMQVSRQASIVIAYAMKE 271
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Db 105 SKQLVHQKMQVSRQASIVIAYAMKE 129

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-8

Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

Qy 28 HIEKPVSVQAMWSAIQ 43
[illegible]
Db 295 HIEKPVSVQAMWSAIQ 310

RESULT 11
US-09-775-925-2-11
; Sequence 11, Application US/09775925
; Publication No. US20020182203A1
; GENERAL INFORMATION:
; APPLICANT: Barbe, Ruth M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: [illegible]
; FILE REFERENCE: 20012%.433
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-11

Query Match [illegible] Score [illegible] DB [illegible] Length [illegible]
Best Local Similarity [illegible] Pred. No. [illegible]
Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

Qy 25 LVEPKMGVSRSA 261
[illegible]
Db [illegible] LVEPKMGVSRSA 91

RESULT 12
US-09-761-640-6
; Sequence 6, Application US/09761640
; Patent No. US20020137042A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 21000964 CIP
; CURRENT APPLICATION NUMBER: US/09/761,640
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Human
US-09-761-640-6

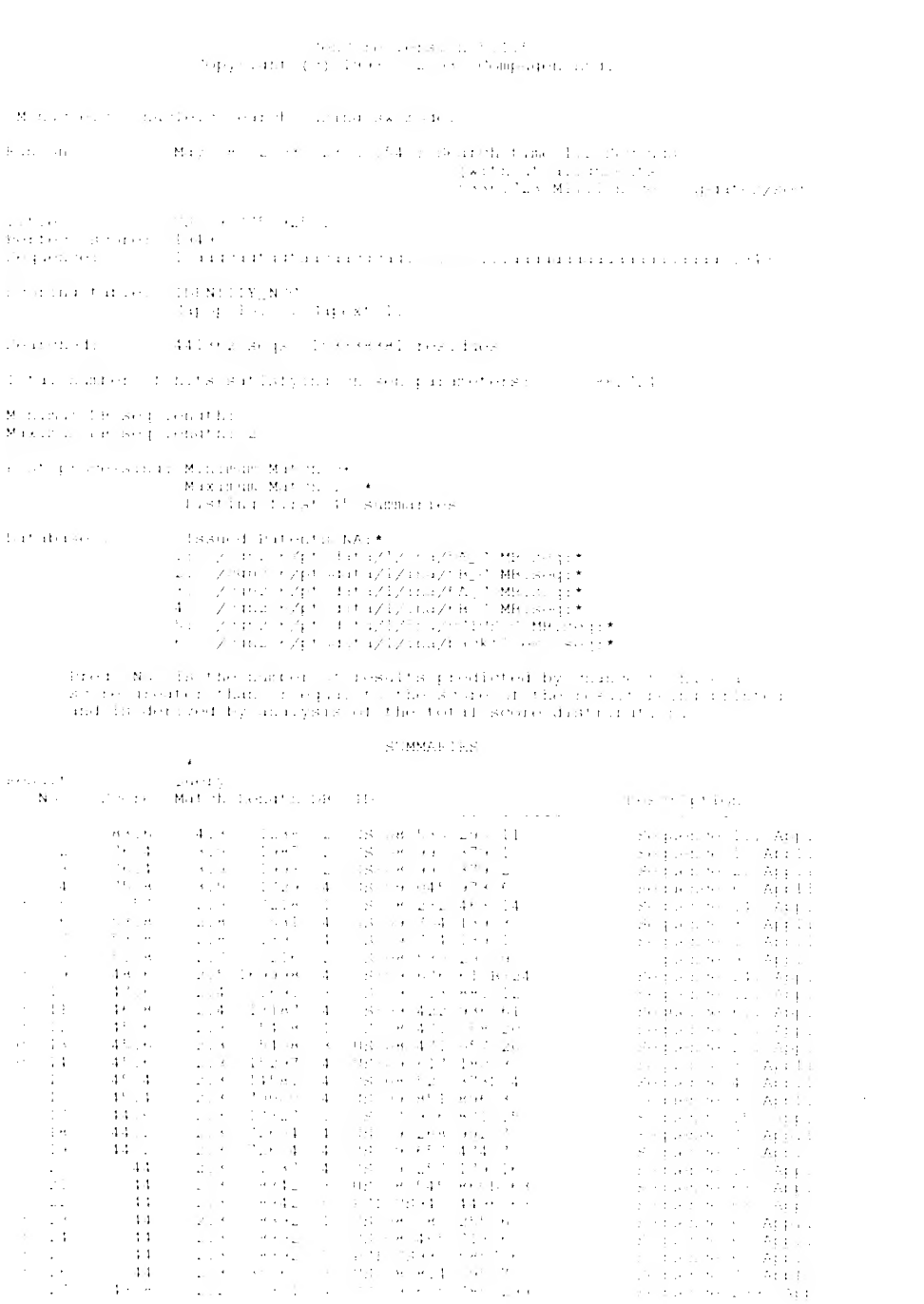
Query Match [illegible] Score [illegible] DB [illegible] Length [illegible]
Best Local Similarity [illegible] Pred. No. [illegible]
Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

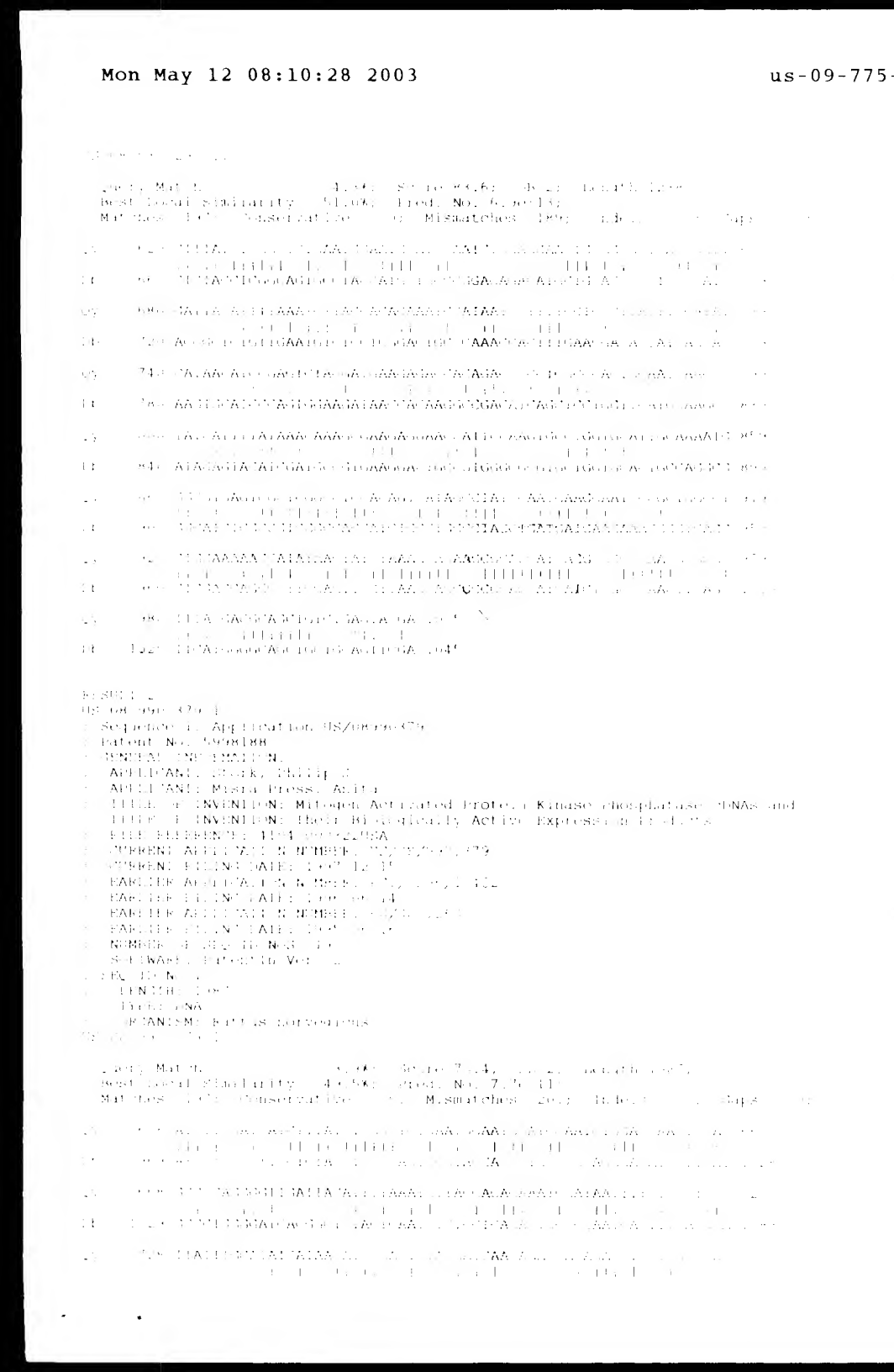
Qy 25 LVEPKMGVSRSA 261
[illegible]
Db 317 LVEPKMGVSRSA 456

RESULT 13
US-09-775-925-21
; Sequence 21, Application US/09775925
; Publication No. US20020182203A1
; GENERAL INFORMATION:
; APPLICANT: Barbe, Ruth M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-1P DUAL SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 20012%.433
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-775-925-21

Query Match [illegible] Score [illegible] DB [illegible] Length [illegible]
Best Local Similarity [illegible] Pred. No. [illegible]
Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

Qy 25 LVEPKMGVSRSA 261
[illegible]

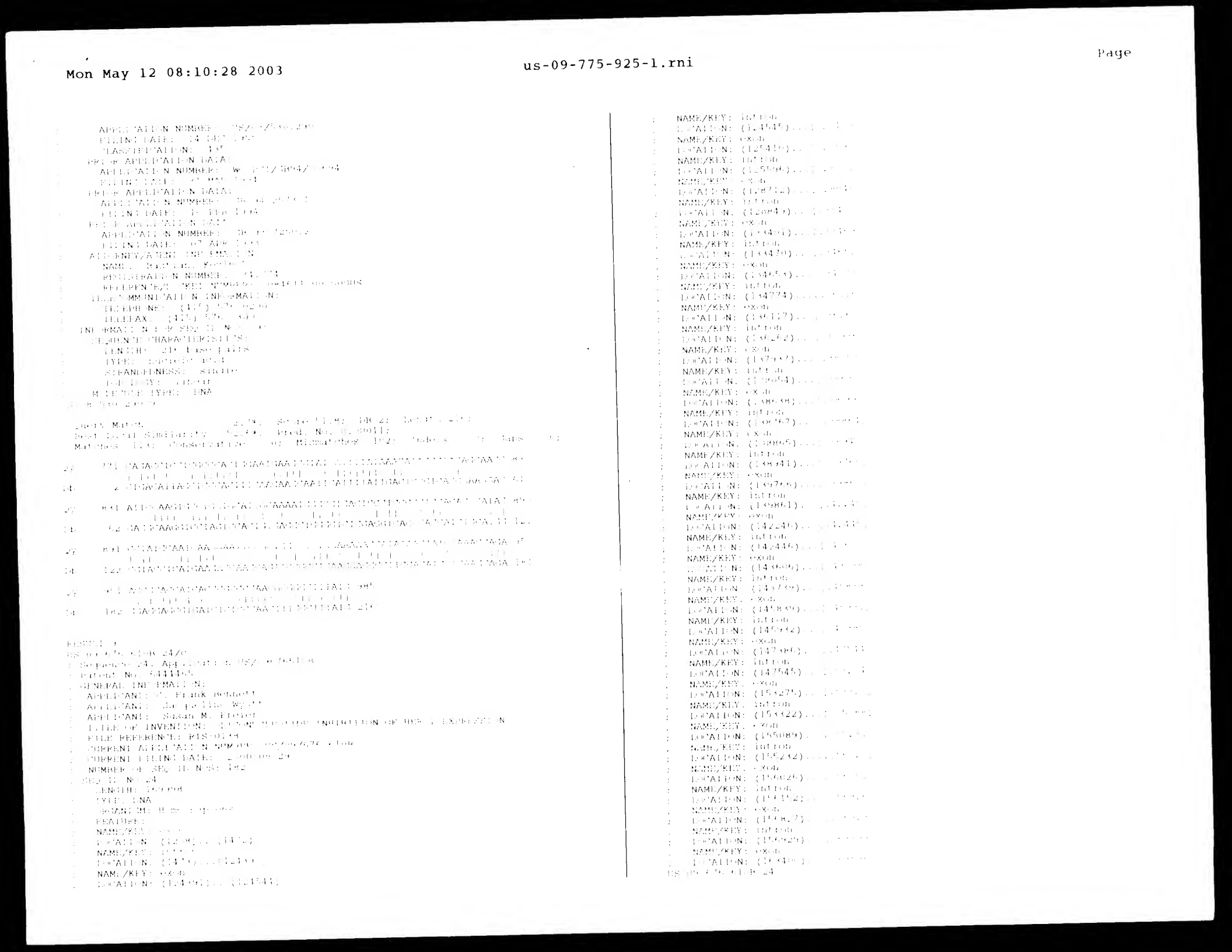


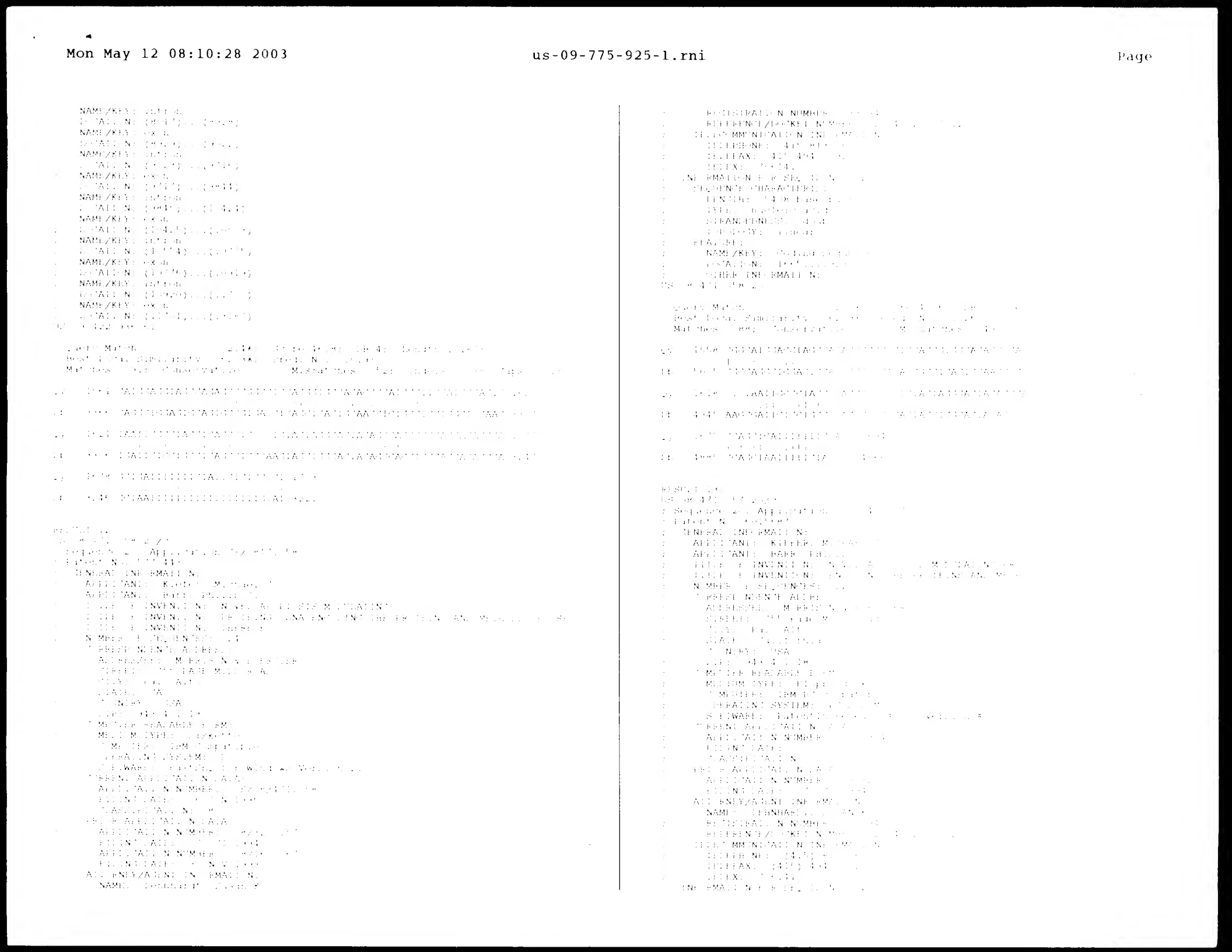


; Sequence 1, Application US/09704139
; Patent No. 6420153
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosalina
; TITLE OF INVENTION: [illegible] A NOVEL DUAL SPECIFICITY PHOSPHATASE AND [illegible] THEREOF
; FILE REFERENCE: 10448-018001
; CURRENT APPLICATION NUMBER: US/09/704,139
; CURRENT FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: US 60/057,772
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (329)..(859)
; NAME/KEY: misc_feature
; LOCATION: (1)..(1599)
; OTHER INFORMATION: n = A, T, G, or C
US-09-704-139-1

Query Match 2.8%; Score 53.8; DB 4; Length [illegible]
Best Local Similarity 49.1%; Pred. No. 8.2e-05;
Matches 142; Conservative 0; Mismatches 147; Indels [illegible]; Gaps [illegible]

RESULT 2
[illegible]
; Sequence 9, Application US/08520295
; Patent No. 5958724
; GENERAL INFORMATION:
; APPLICANT: Marshall, Christopher John
; APPLICANT: Ashworth, Alan
; APPLICANT: Hughes, David Anthony
; TITLE OF INVENTION: Methods for Screening of Substances for
; TITLE OF INVENTION: Therapeutic Activity and Test Kits Therefor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.[illegible]
; CURRENT APPLICATION DATA:





; SEQUENCE CHARACTERISTICS:
; LENGTH: 5438 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1665..1928
US-08-471-057-2

Query Match ... 3.6%; Score 57.6; DB 4; Length 5438;
Best Local Similarity ... 62.9%; Pred. No. 0.015;
Matches ... 85; Conservative ... 0; Mismatches ... 51; Indels ... 0; Gaps ... 1;

Qy 1556 ... 1615
Db 5005 ... 5064

Qy 1616 ... 1675
Db 4945 ... 4886

RESULT 13
US-09-817-180-4
; Sequence 4, Application US/09817180
; Patent No. ...5504
; GENERAL INFORMATION:
; APPLICANT: SUN, Weidong et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: A ... 107 ... DNA ...
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001184
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ... Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 15247
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-4

Query Match ... 2.3%; Score 45.6; DB 4; Length 15247;
Best Local Similarity ... 61.5%; Pred. No. 0.054;
Matches ... 96; Conservative ... 0; Mismatches ... 54; Indels ... 0; Gaps ... 1;

Qy 1561 ... 1620
Db 12204 ... 12145

Qy 1621 ... 1675
Db 12144 ... 12117

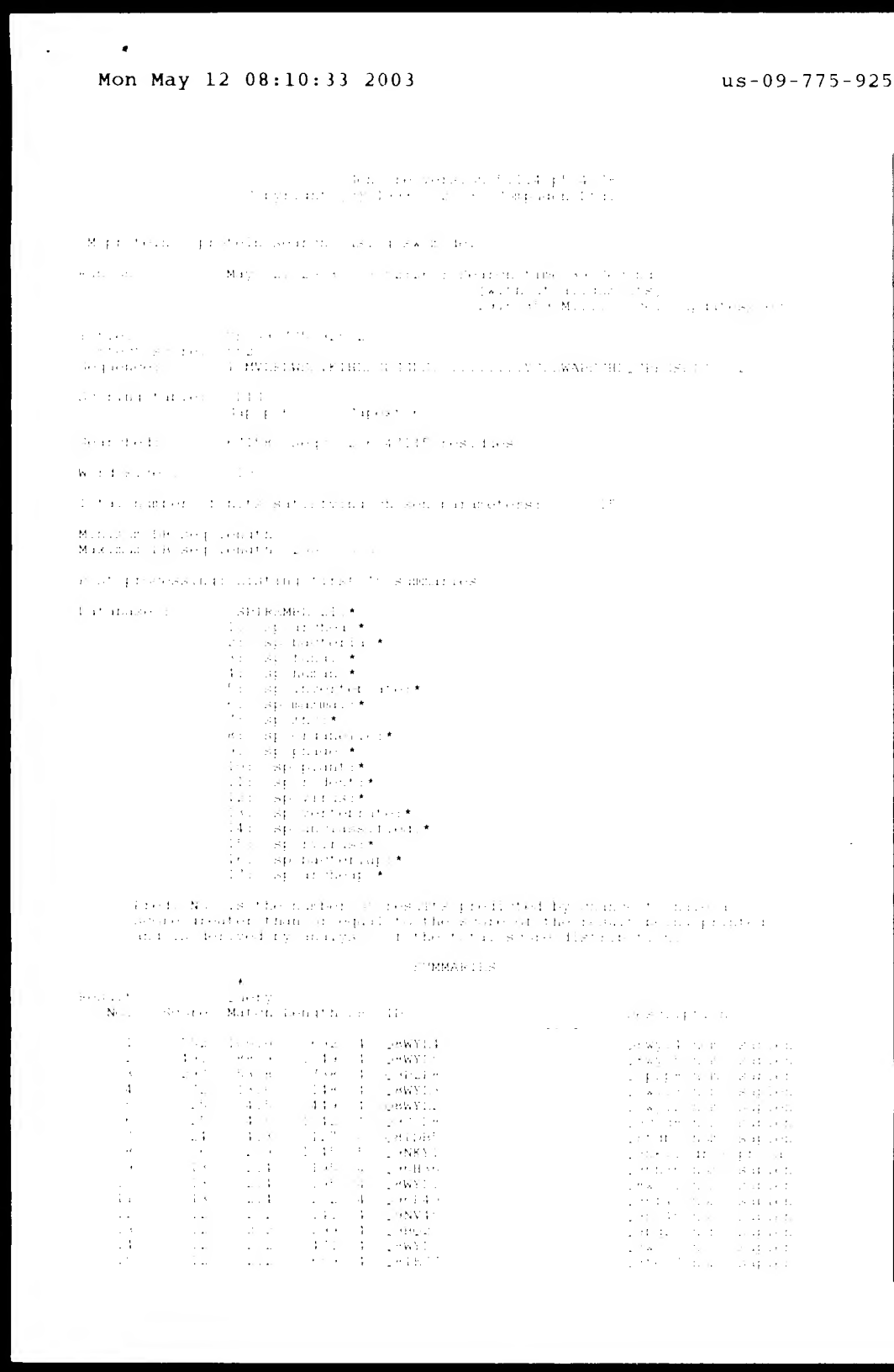
RESULT 15
US-08-920-037A-1
; Sequence 1, Application US/08920037A
; Patent No. 5451763
; GENERAL INFORMATION:
; APPLICANT: Tomkins Link, Joyce
; APPLICANT: Stoerker, Florian B
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
; FILE REFERENCE: 2926.420USD1
; CURRENT APPLICATION NUMBER: US/08/920,037A
; CURRENT FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,079
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/994,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 14581
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: EXON; 6581..6750; EXON 11594..11675;
; OTHER INFORMATION: EXON; 14579..14581; INTRON; 6751..11583; INTRON;
; OTHER INFORMATION: 11676..14578; CDS; 11584..11675; 14579..14581
US-08-920-037A-4

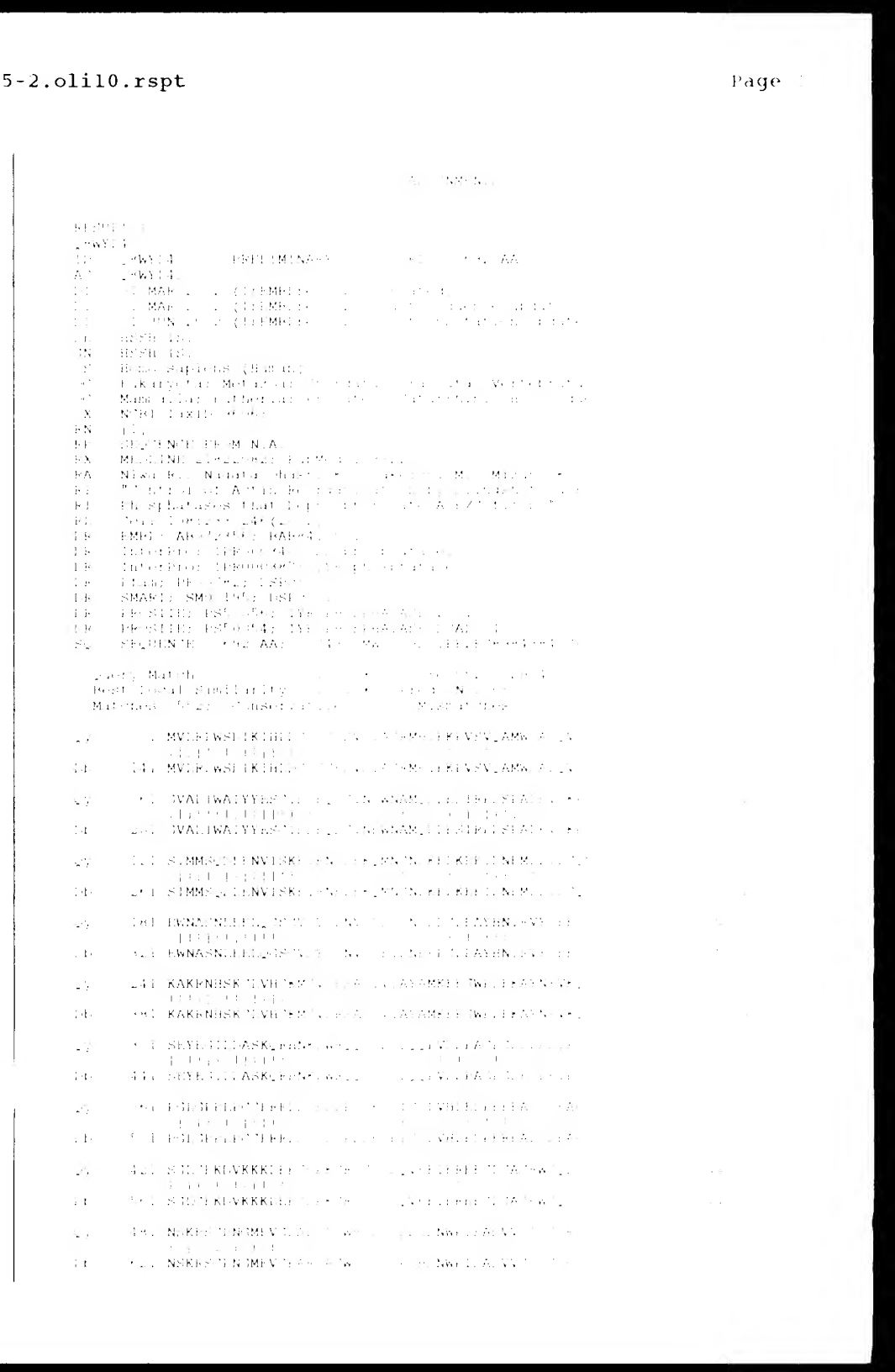
Query Match ... 2.3%; Score 45.4; DB 4; Length 14581;
Best Local Similarity ... 59.7%; Pred. No. 0.049;
Matches ... 95; Conservative ... 0; Mismatches ... 64; Indels ... 4; Gaps ... 2;

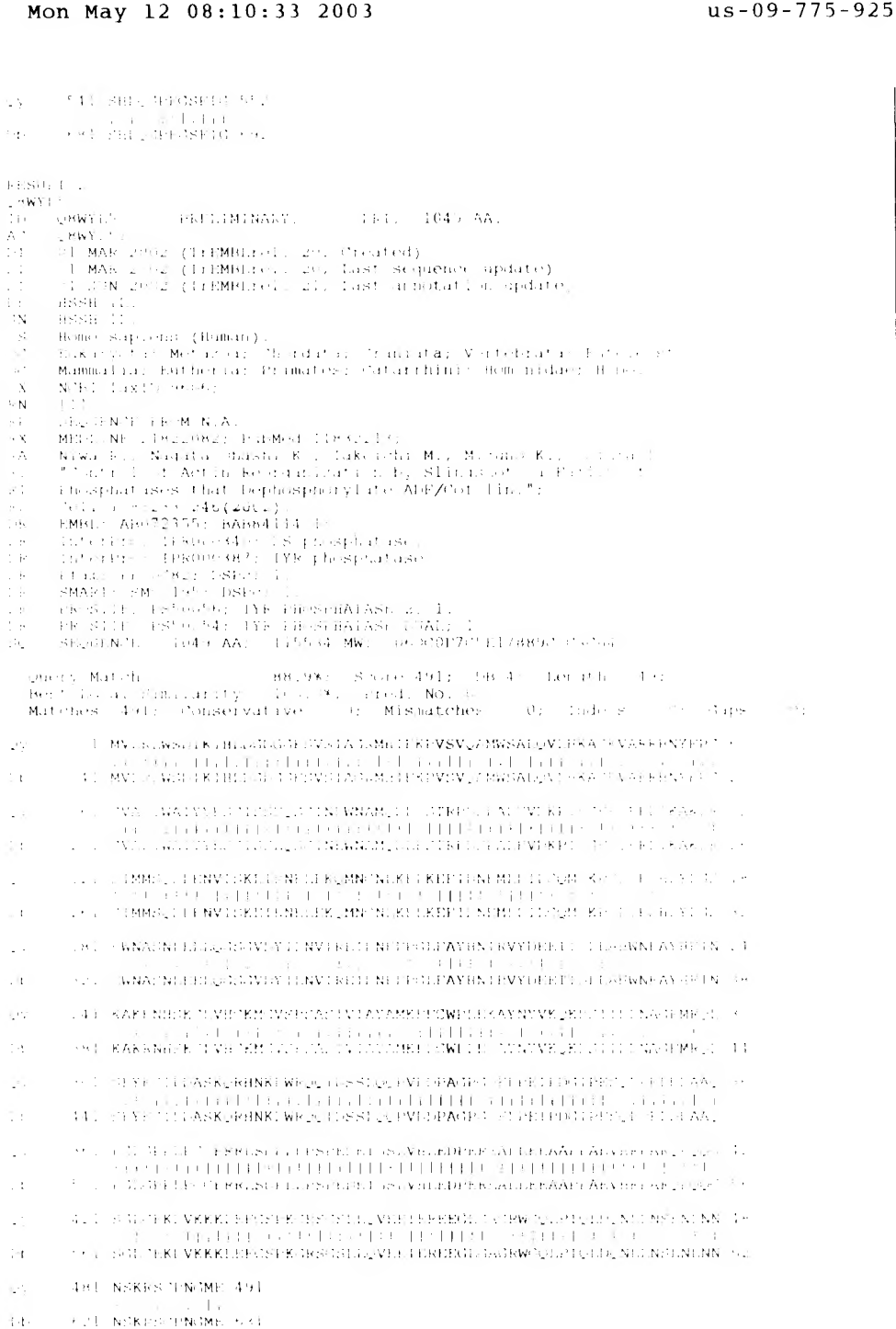
Qy 1561 ... 1620
Db 11674 ... 11733

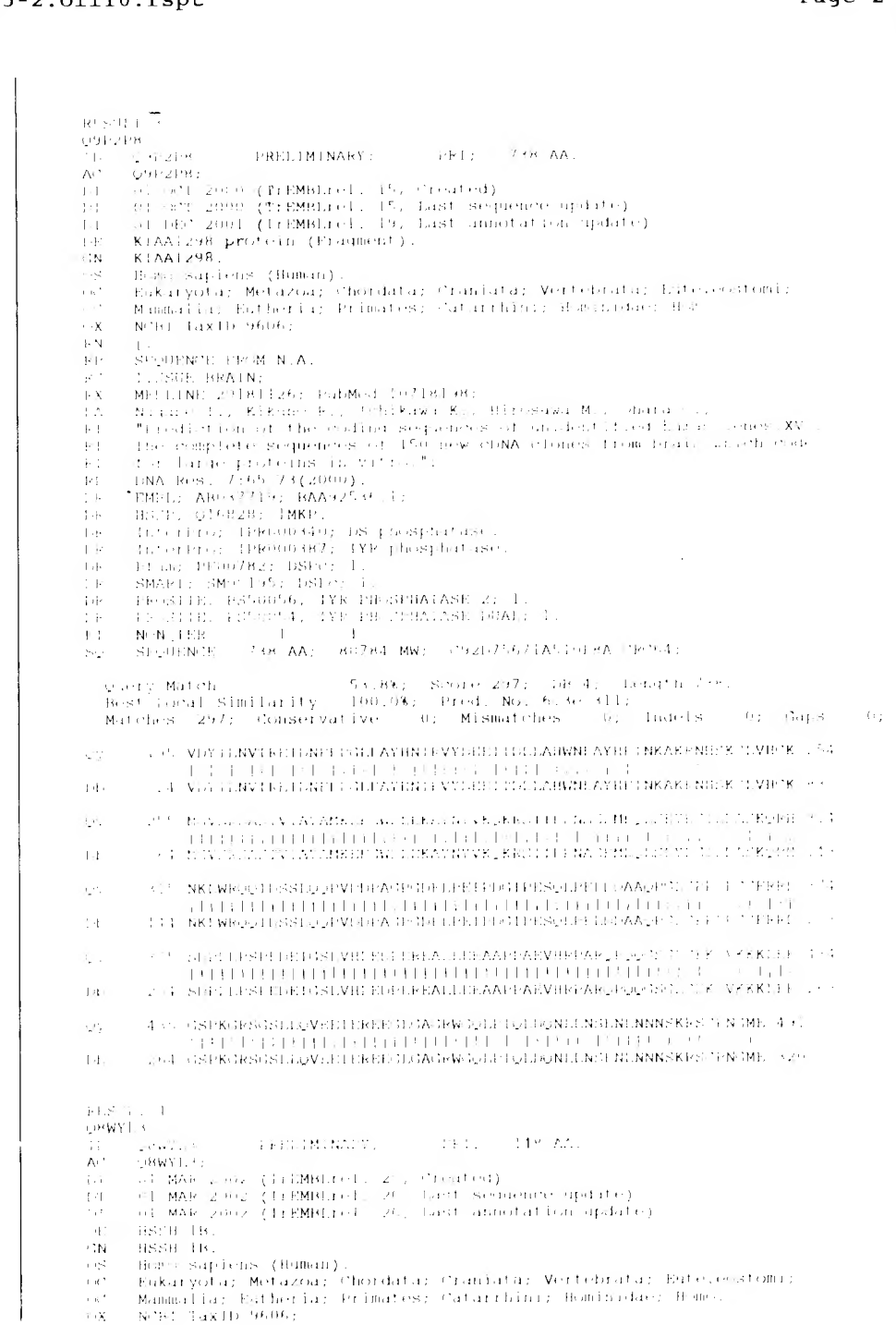
Qy 1621 ... 1675
Db 11734 ... 11787

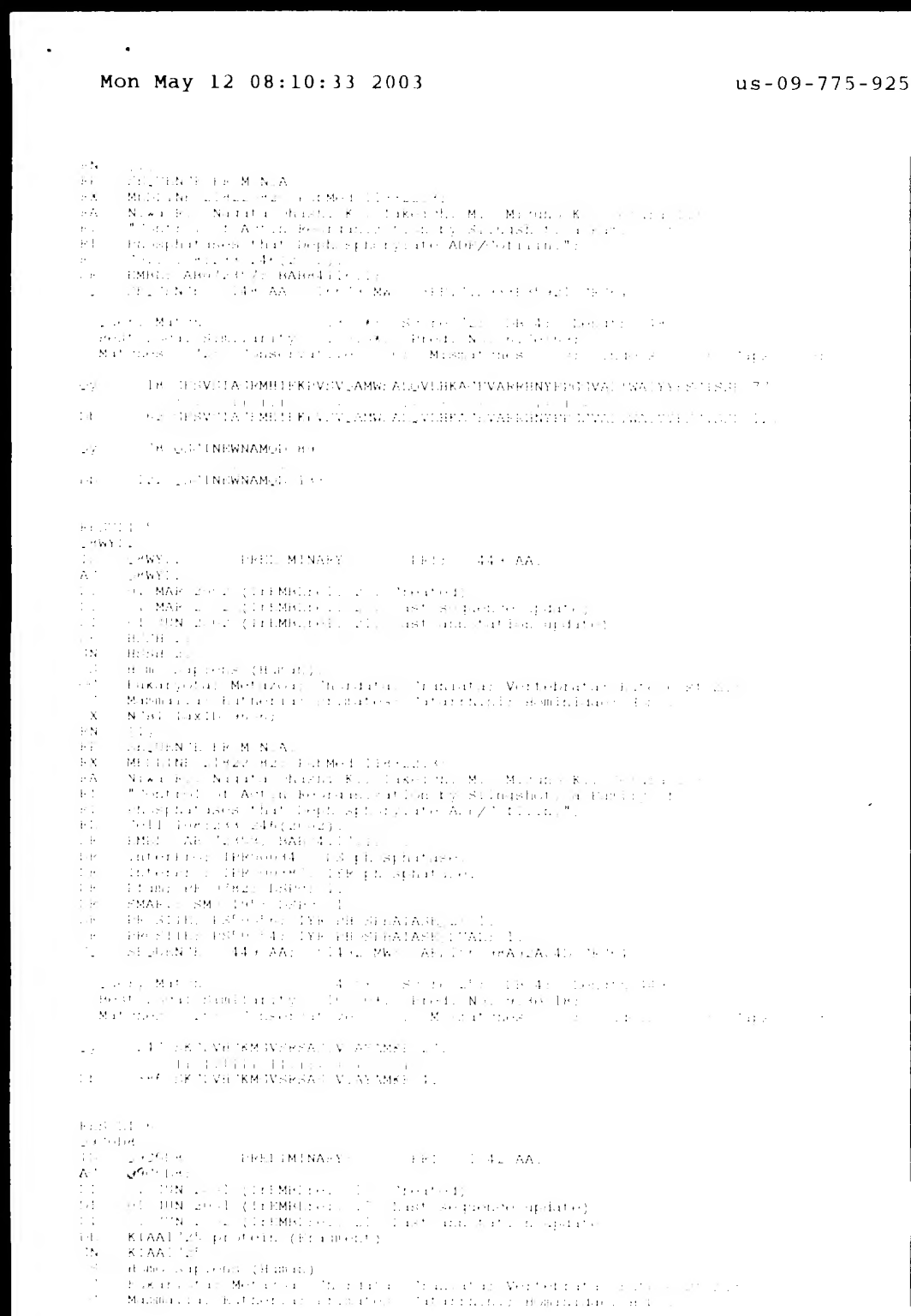
Search completed: May 9, 2003, 03:45:28
Job time : 550 secs

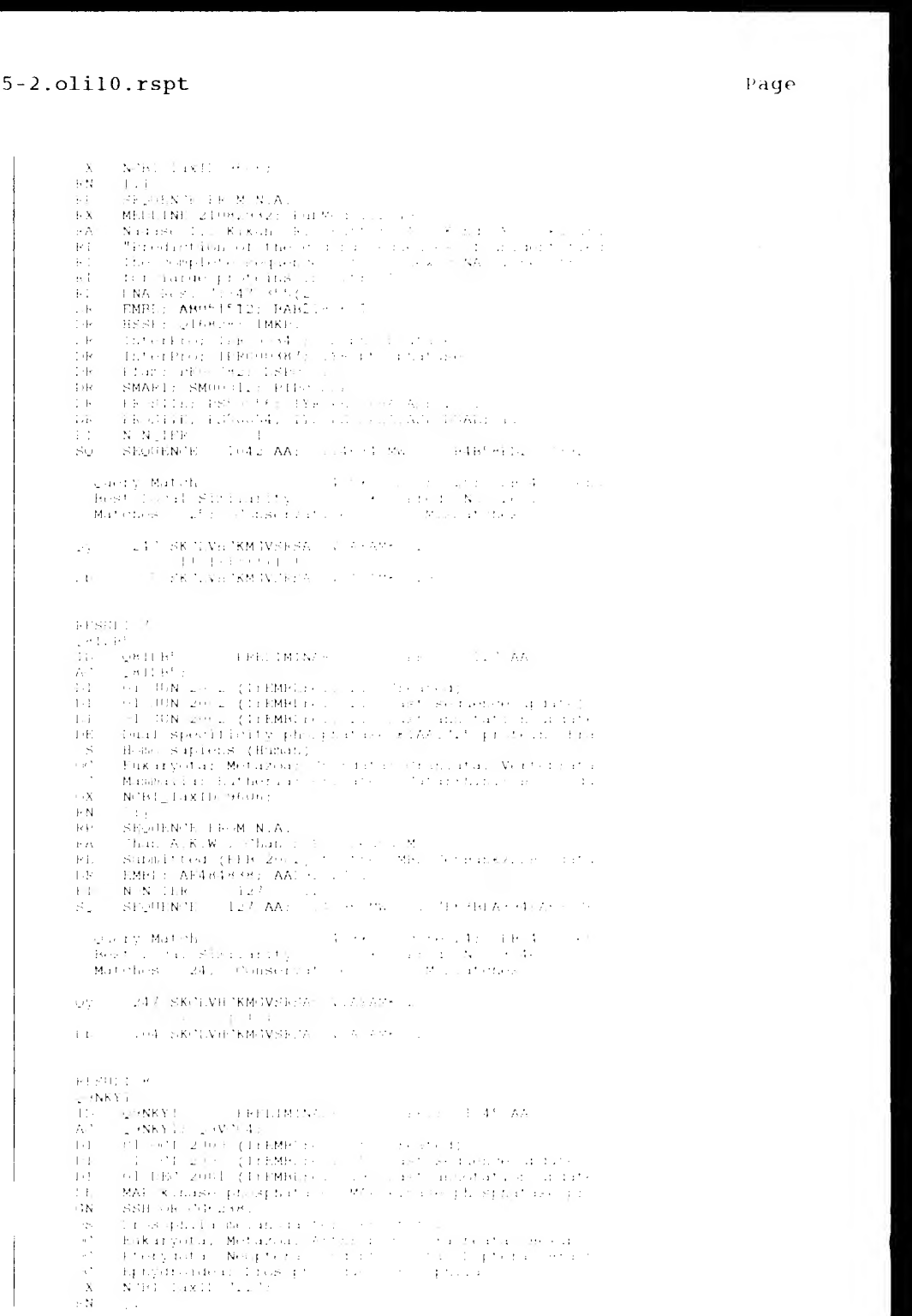












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SQ   SEQUENCE FROM N.A.
RA   Nishi K., Takeuchi M., Yamada T.;
RT   "A novel MAP kinase phosphatase (Drosophila).";
RL   Submitted (JAN 2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY
RA   Mural R.J., Adams M.D., Myers E.W., Smith H.O., Miklos G.L.G.,
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA   Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S.,
RA   Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M.,
RA   Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P.,
RA   Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R.,
RA   Houston J., Hostin D., Houston K.A., Howland T.J., Wei M.-H.,
RA   Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,
RA   Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S.,
RA   Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.,
RA   Li Z., Liang Y., Lin X., Liu X., Mattei B., Mcintosh T.C.,
RA   Mcleod M.P., Mcpherson D., Merkulov G., Milshina N.V., Mobarry C.,
RA   Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B.,
RA   Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A.,
RA   Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S.,
RA   Pan S., Pollard J., Puri V., Reese M.G., Reinert K.,
RA   Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Sidén-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H.,
RA   Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M.,
RA   Weissenbach J., Williams S.M., Woodage T., Worley K.C.,
RA   Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S.,
RA   Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H.,
RA   Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA   Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AF306784; AAK06784.1; -.
DR   EMBL; AF279571; AAF50372.2; -.
DR   HSSP; Q16827; 1MKP.
DR   FlyBase; FBgn0029157; ssh.
DR   InterPro; IPR000340; DSP_phosphatase.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase.
SQ   SEQUENCE   195 AA;  21967 MW;  2FB6C284CB49E4C0 CRC64;

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 IHLIPGGFSVSI 26
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Db     174 IHLIPGGFSVSI 162


RESULT 2
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DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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GN   HSSB 2A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22322682; PubMed=11932317;
RA   Nishi K., Nagata-Ohashi K., Takeuchi M., Mizuno K., Suzuki T.,
RT   "Control of Actin Reorganization by Slingshot, a Family of
RT   Phosphatases that Dephosphorylate ADF/Cofilin.";
RL   Cell 108:233-246(2002).
DR   EMBL; AB072859; BAB84118.1; -.
SQ   SEQUENCE   195 AA;  21661 MW;  EB541D27D8B7A250 CRC64;

  Query Match             2.4%;  Score 15;  DB 4;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 IHLIPGGFSVSI 26
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Db     174 IHLIPGGFSVSI 162


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DT   01-DEC-2000 (TrEMBLrel. 13, Created)
DT   01-DEC-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2000 (TrEMBLrel. 13, Last annotation update)
DE   Putative (protein for MGC:12915).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Strausberg R.;
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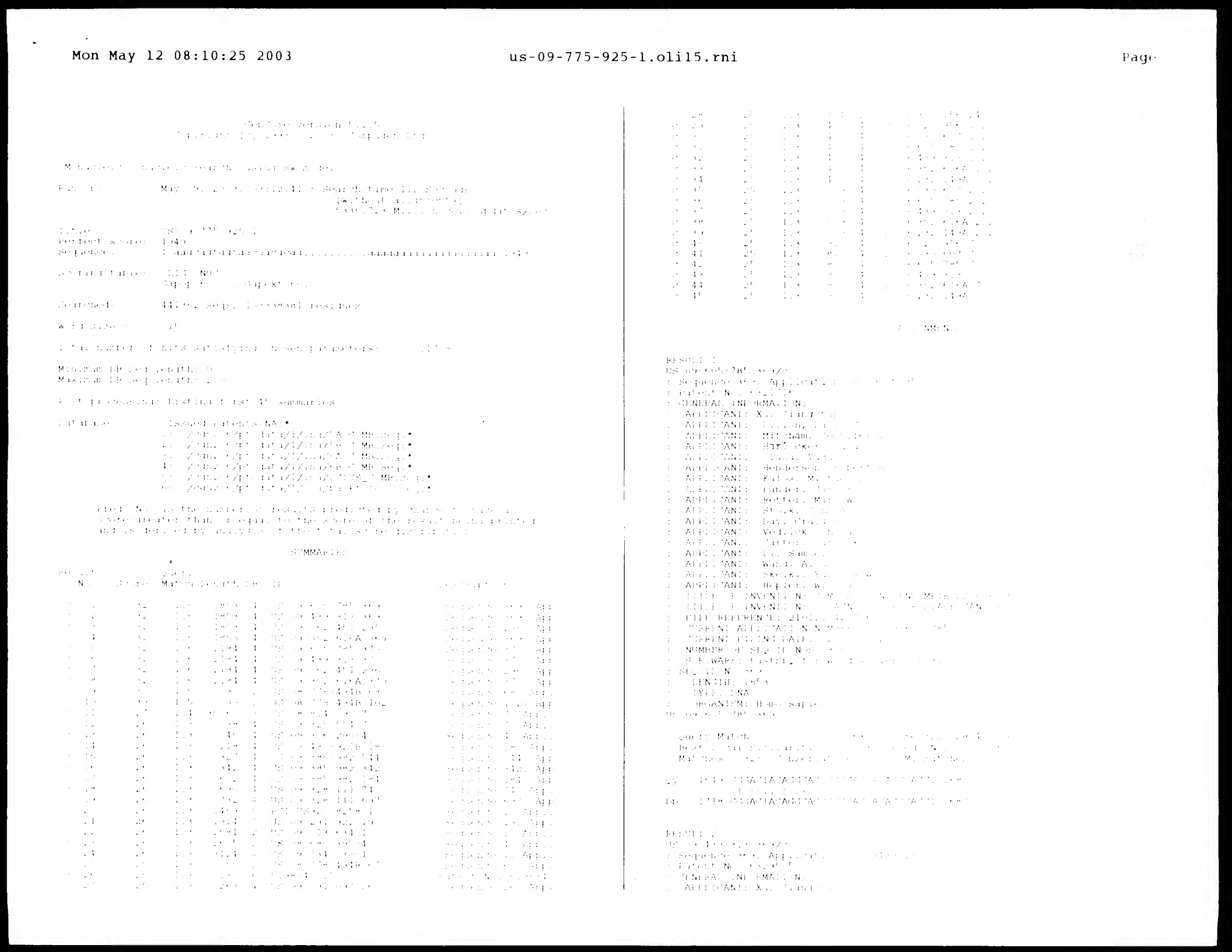

```
  APPLICANT:  Dillon, David C.
  APPLICANT:  Mitcham, Jennifer L.
  APPLICANT:  Barlocker, Susan Louise
  APPLICANT:  Jiang, Yuqui
  APPLICANT:  Xu, Jiangchun
  APPLICANT:  Kolb, Steven G.
  APPLICANT:  Kolb, Michael
  APPLICANT:  Fangmeier, Gary
  APPLICANT:  Bottger, Mark
  APPLICANT:  Stolk, John
  APPLICANT:  Day, Craig
  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC
  TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
  FILE REFERENCE: Z10121.42C9
  CURRENT APPLICATION NUMBER: US/09/775,925
  CURRENT FILING DATE: 1999-11-12
  NUMBER OF SEQ ID NOS: 975
  SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 969
  LENGTH: 1853
  TYPE: DNA
  ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature

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  Best Local Similarity   100.0%;  Pred. No. 0.00013;
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Db     1756 GGGACTACAGGCACCCGCCACACACCCAGCT 1796


RESULT 4
US-09-775-925-1
; Sequence 969, Application US/09775925
; Patent No. 6344550
; GENERAL INFORMATION:
;  APPLICANT:  Prodromou, Tony N.
;  APPLICANT:  Smith, John M.
;  APPLICANT:  Reed, Steven I.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF BREAST CANCER
;  NUMBER OF SEQUENCES:  20
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  SEED and Berry LLP
;    STREET:  6300 Columbia Center, 701 Fifth Avenue
;    CITY:  Seattle
;    STATE:  Washington
;    COUNTRY:  USA
;    ZIP:  98104-7092
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Floppy disk
;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/09/775,925
;    FILING DATE:  04-Feb-2001
;    CLASSIFICATION:
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  Mak, David C.
;    REGISTRATION NUMBER:  42,778
;    REFERENCE/DOCKET NUMBER:  21121.1502
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  (206) 622-4900
;    TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  969:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1853 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-775-925-969

  Query Match                 1.9%;  Score 32;  DB 4;  Length 1853;
  Best Local Similarity   100.0%;  Pred. No. 0.00013;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1640 GGGACTACAGGCACCCGCCACACACCCAGCT 1680
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Db     1756 GGGACTACAGGCACCCGCCACACACCCAGCT 1796


RESULT 5
US-09-775-925-970
; Sequence 970, Application US/09775925
; Patent No. 6342216
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, David C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Barlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kolb, Michael D.
;  APPLICANT:  Fangmeier, Gary R.
;  APPLICANT:  Bottger, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Ji, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skelly, Yasir A.W.
;  APPLICANT:  Depler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: Z10121.42C16
;  CURRENT APPLICATION NUMBER: US/09/775,925
;  CURRENT FILING DATE:  2000-06-27
;  NUMBER OF SEQ ID NOS: 975
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 970
;   LENGTH: 2161
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Software Check, Inc. d/b/a SoftwareChek
; STREET: 1521 N.W. 41st Street, Suite A
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32605
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: PatentIn Release #1.0, Version # 1.30
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,925
; FILING DATE: 03-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/582,562
; FILING DATE: 03-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: CL 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 1
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-775-925-1

Query Match 1.5%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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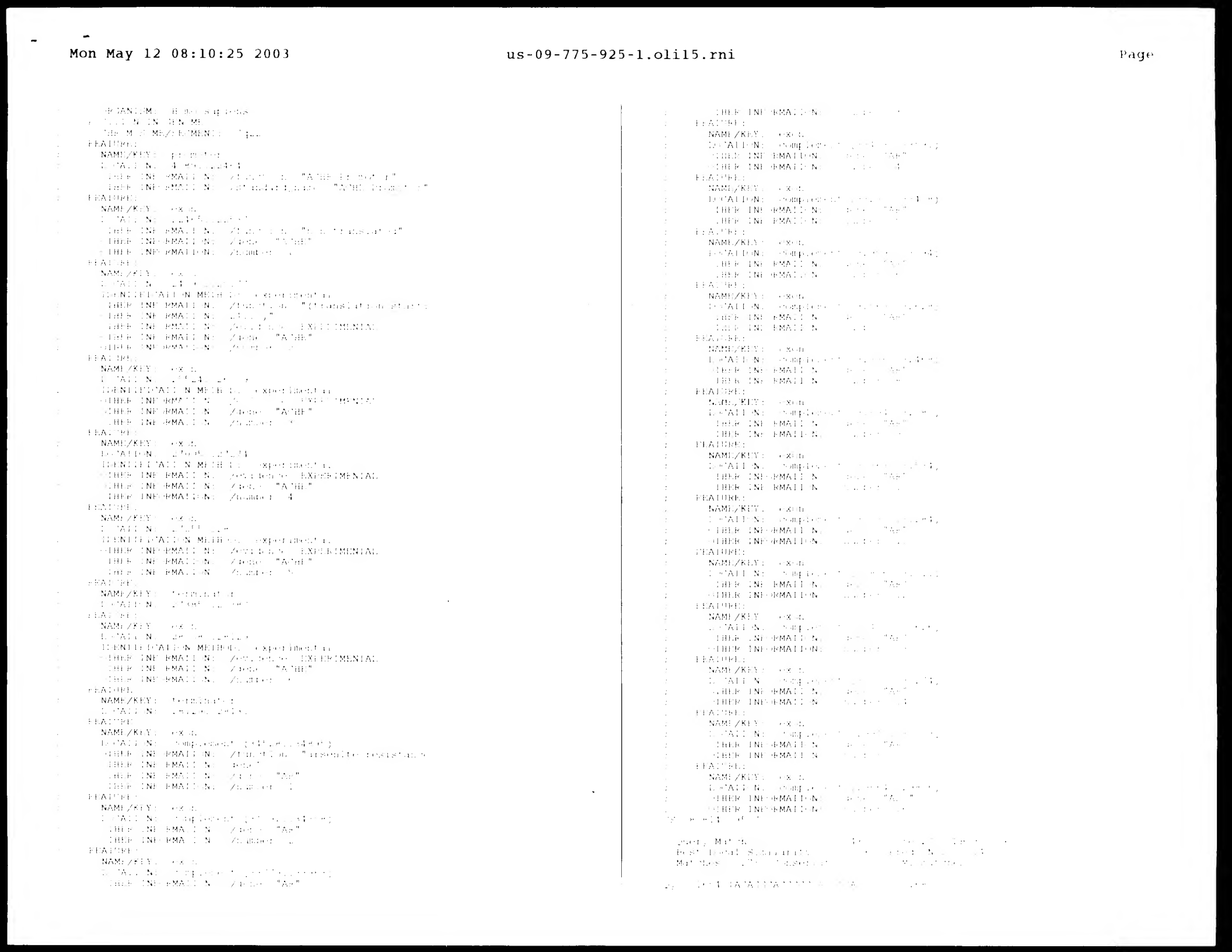
RESULT 2
US-08-814-095-2
; Sequence 2, Application US/08814095
; Patent No. 5625184
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: ANTISENSE ACHE OLIGONUCLEOTIDES AND ASSOCIATED METHODS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 Northwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohamadi, Ilissa N.
; REGISTRATION NUMBER: 39,972
; REFERENCE/DOCKET NUMBER: 2691.00006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4000 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Cosmid including ACHE
; CONSTRUCTION: promoter, ACHE gene and AES gene"
; IMMEDIATE: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:



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RESULT 12
US [illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. 6410235
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Kurt
;  APPLICANT: Brand, Joachim
;  TITLE OF INVENTION: DNA DETECTION BY MEANS OF A STRAND [illegible]
;  FILE REFERENCE: 024420 [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible],554
;  CURRENT FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: DE 198 24 900.4
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn version [illegible]
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;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
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;   NAME/KEY: misc_signal
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;   OTHER INFORMATION: [illegible]
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RESULT 13
US-09-[illegible]-4/[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Rovera, Giovanni
;  APPLICANT: Mukhopadhyay, [illegible]
;  TITLE OF INVENTION: METHODS FOR [illegible] PHASE AMPLIFICATION [illegible] DNA TEMPLATE
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]9924 [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible] 290
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 4[illegible]
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: [illegible]
;   OTHER INFORMATION: FR28[illegible]
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  Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
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; Sequence 18, Application US/09480921B
; Patent No. 6387637
; GENERAL INFORMATION:
;  APPLICANT: Levin, Joshua Z.
;  APPLICANT: Budziszewski, Gregory J.
;  APPLICANT: Potter, Sharon L.
;  APPLICANT: Wesrlen, Lynette M.
;  TITLE OF INVENTION: Herbicide Target Genes and Methods
;  FILE REFERENCE: PB/5 30780A
;  CURRENT APPLICATION NUMBER: US/09/480,921B
;  CURRENT FILING DATE: 2000-01-11
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 218
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(218)
;   OTHER INFORMATION: n = a, t, c or g
US-09-480-921B-18

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  Best Local Similarity 100.0%; Pred. No. 0.057;
  Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
US-09-[illegible]082-544/c
; Sequence 544, Application US/09[illegible]082
; Patent No. 6262334
; GENERAL INFORMATION:
;  APPLICANT: ENDEGE, WILSON O., ET AL.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS: II
;  FILE REFERENCE: CCDNA 260XX
;  CURRENT APPLICATION NUMBER: US/09/[illegible],082
;  CURRENT FILING DATE: 1999-[illegible]
;  EARLIER APPLICATION NUMBER: [illegible]/[illegible],[illegible]
;  EARLIER FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: [illegible]/[illegible],[illegible]
;  EARLIER FILING DATE: 1999-0[illegible]-27
;  EARLIER APPLICATION NUMBER: [illegible]/[illegible],[illegible]
;  EARLIER FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 544
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 544
;   LENGTH: 327
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
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;   OTHER INFORMATION: n = A,T,C or G
US-09-[illegible]082-544

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  Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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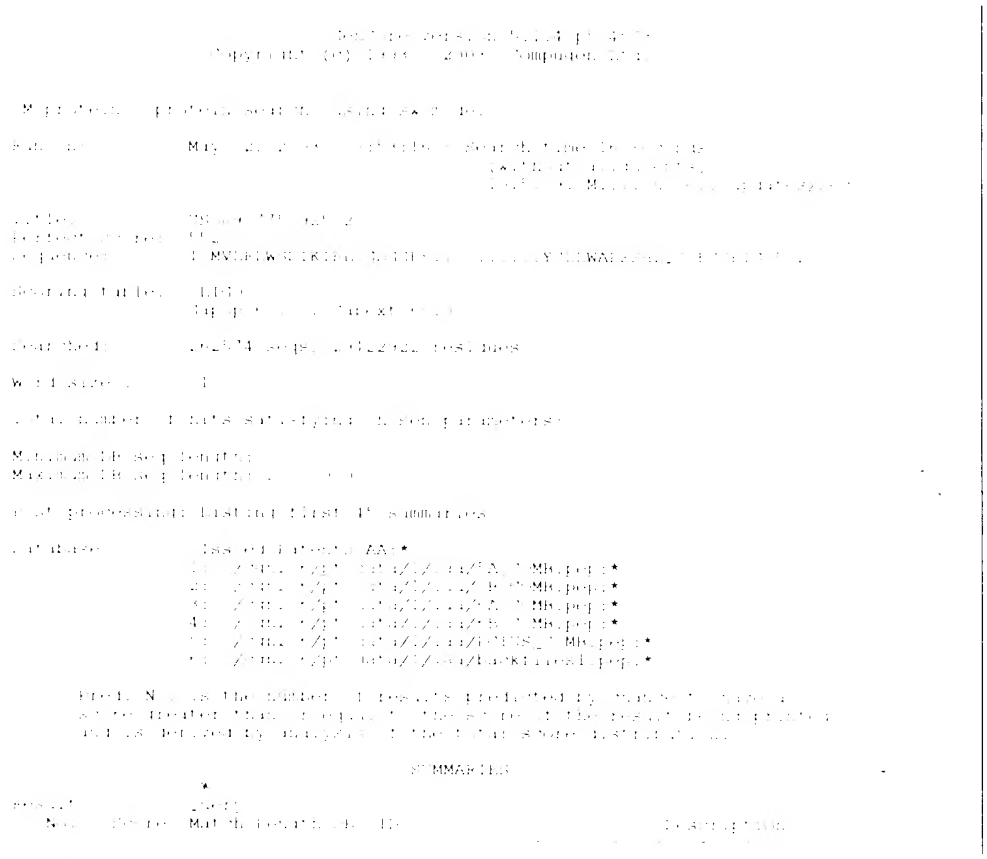

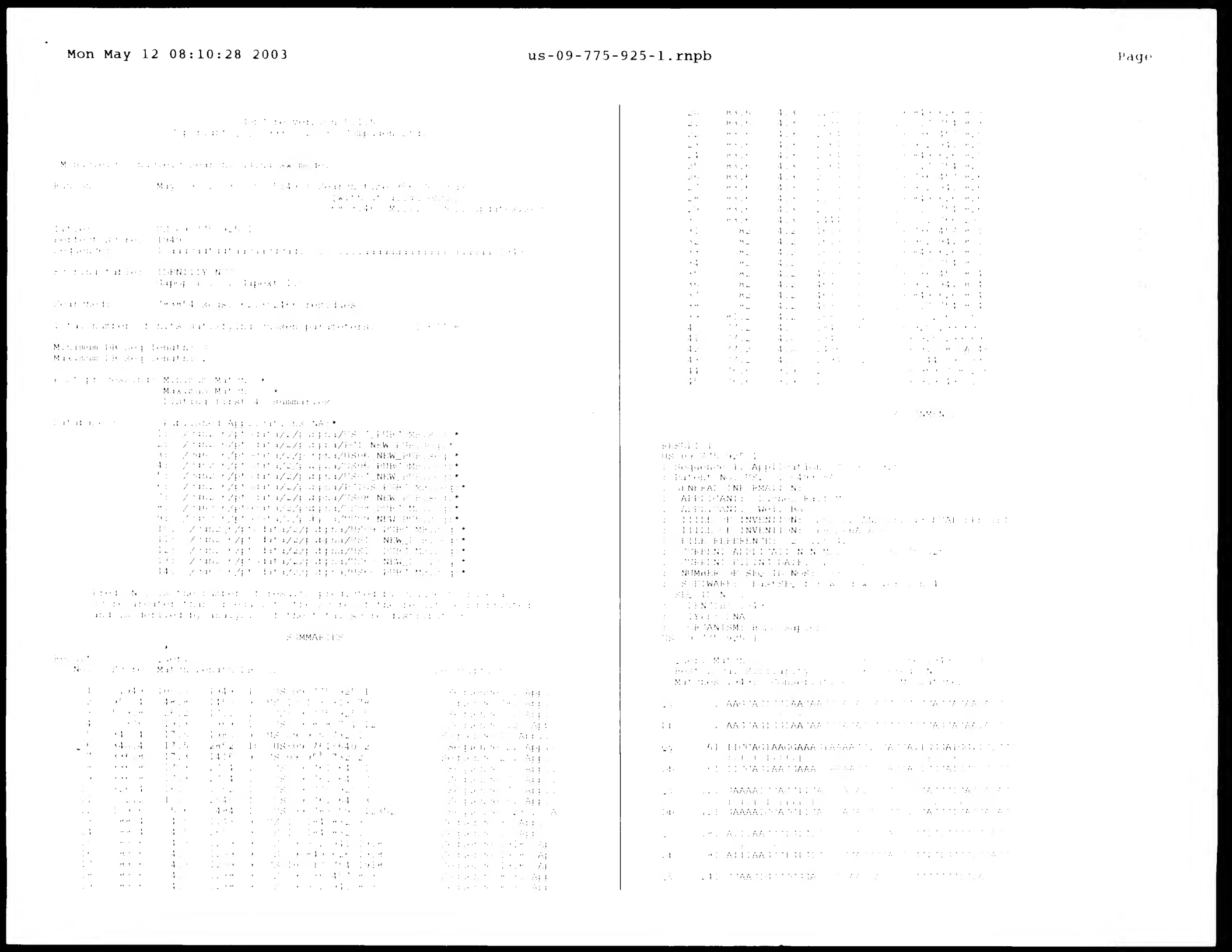

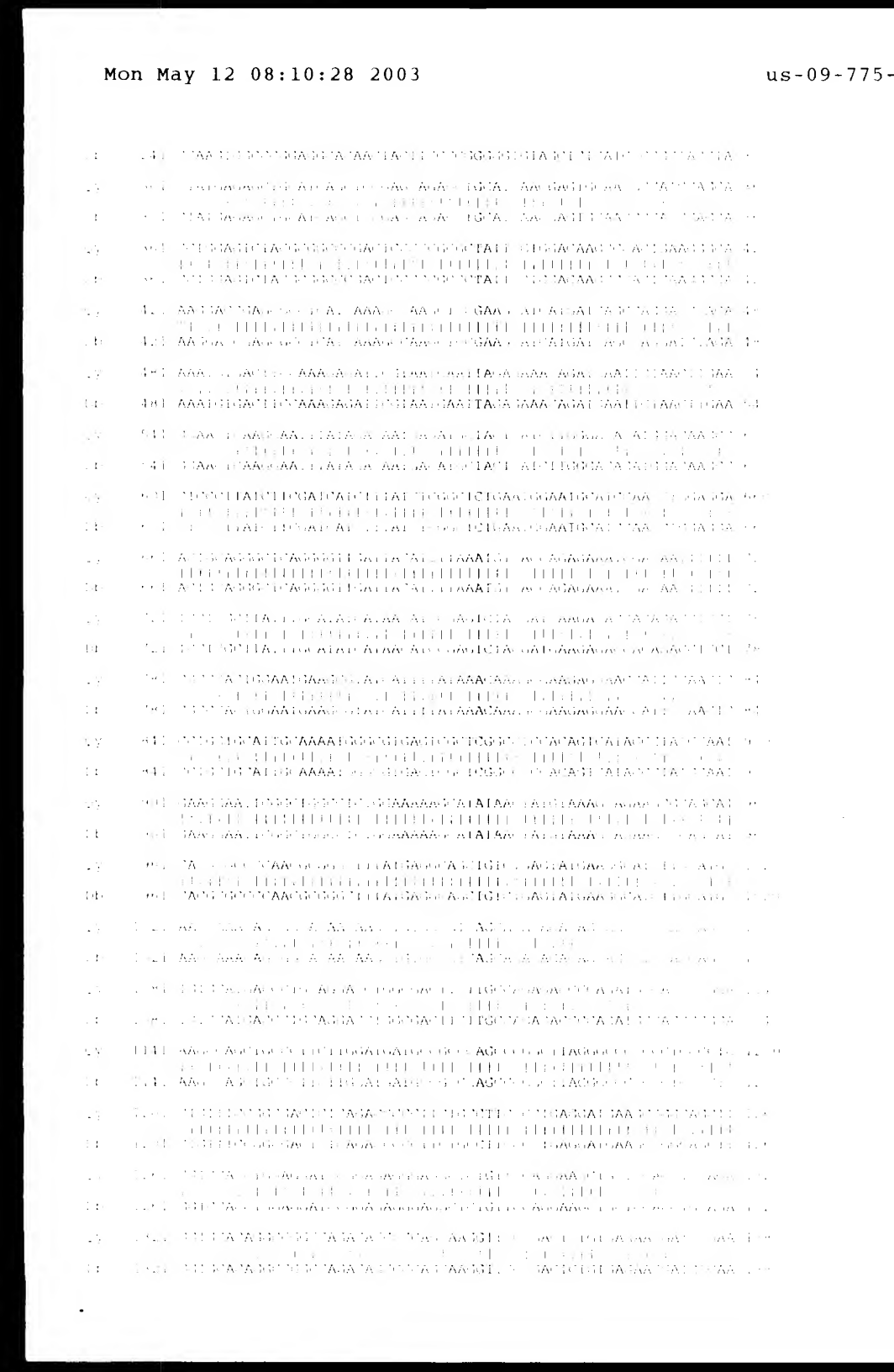

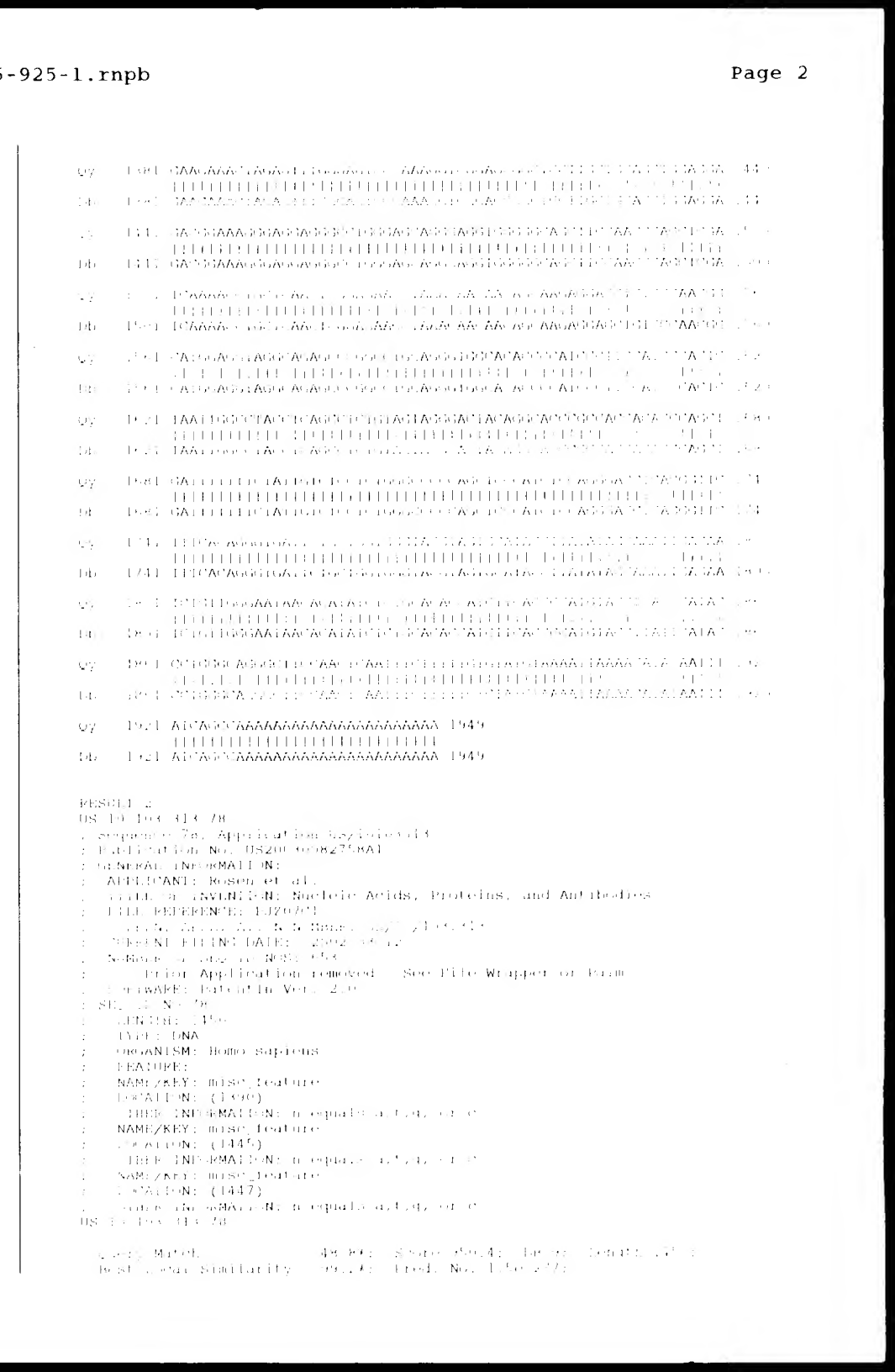

RESULT 2
US-10-103-813-78
; Sequence 78, Application 09/775941
; Publication No. US2001-0008748A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: LJZ067
; CURRENT APPLICATION NUMBER: 09/775,925
; CURRENT FILING DATE: 2001-02-02
; NUMBER OF SEQ IDS: 458
; Prior Application removed - See File Wrapper or Form
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..900)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1445)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1447)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-103-813-78

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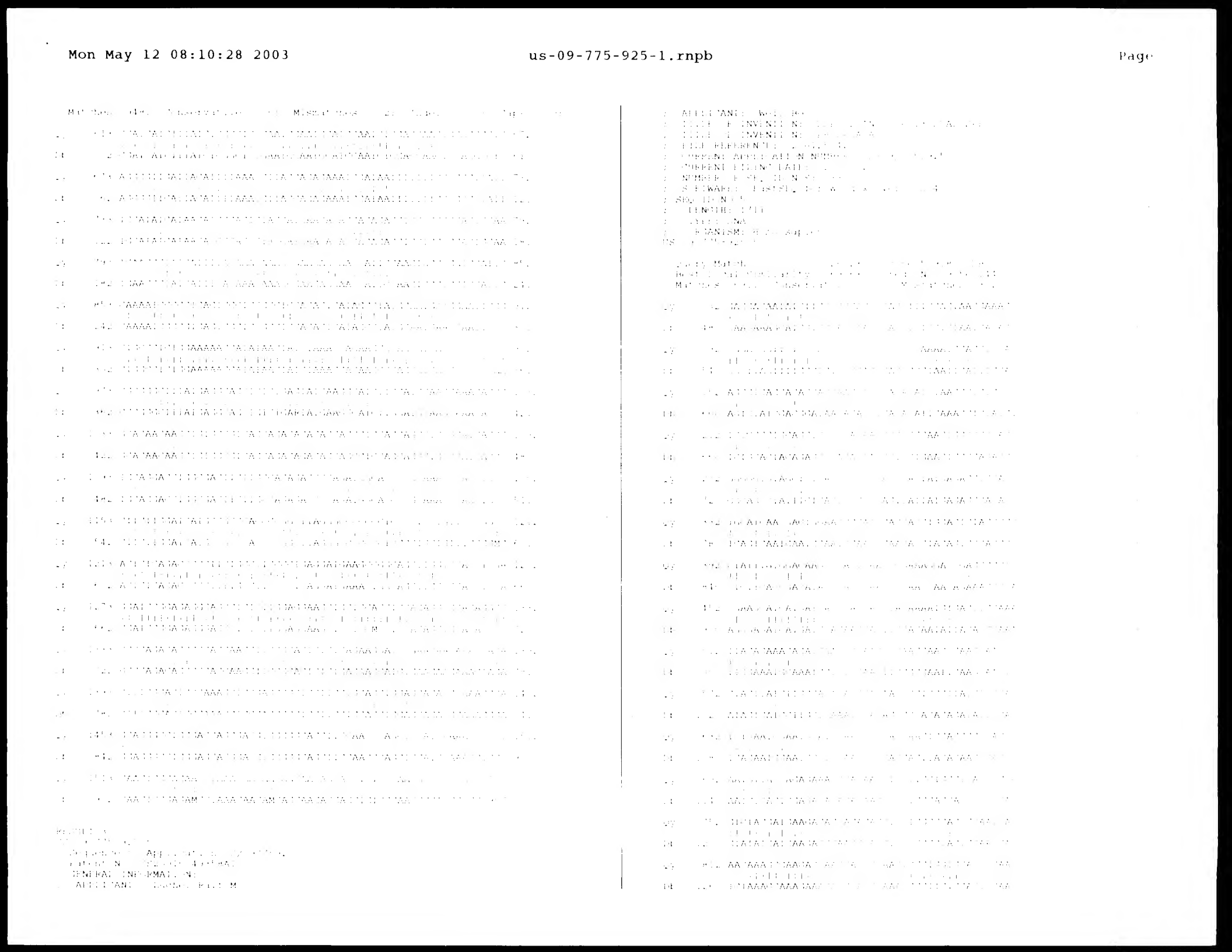

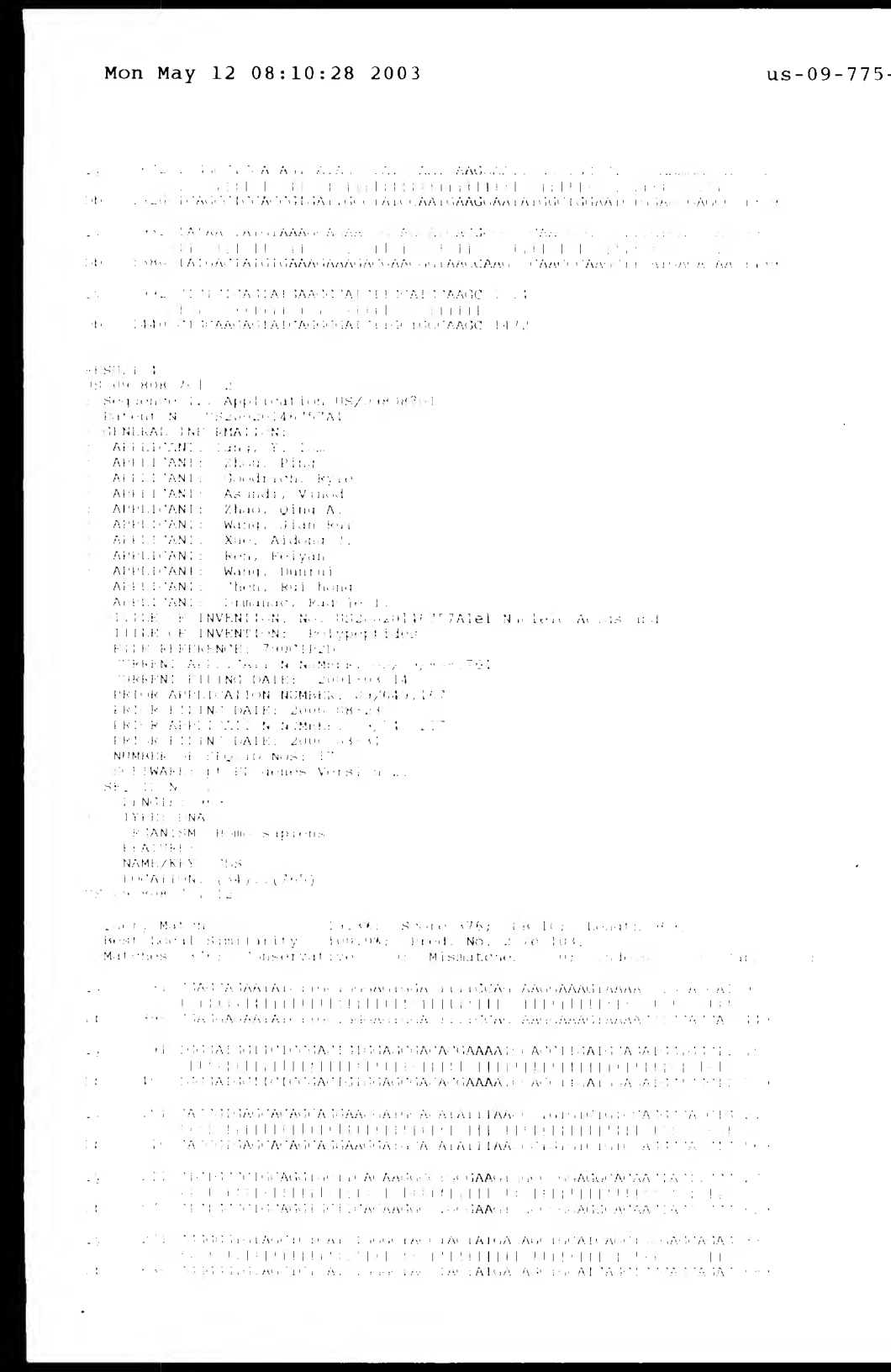

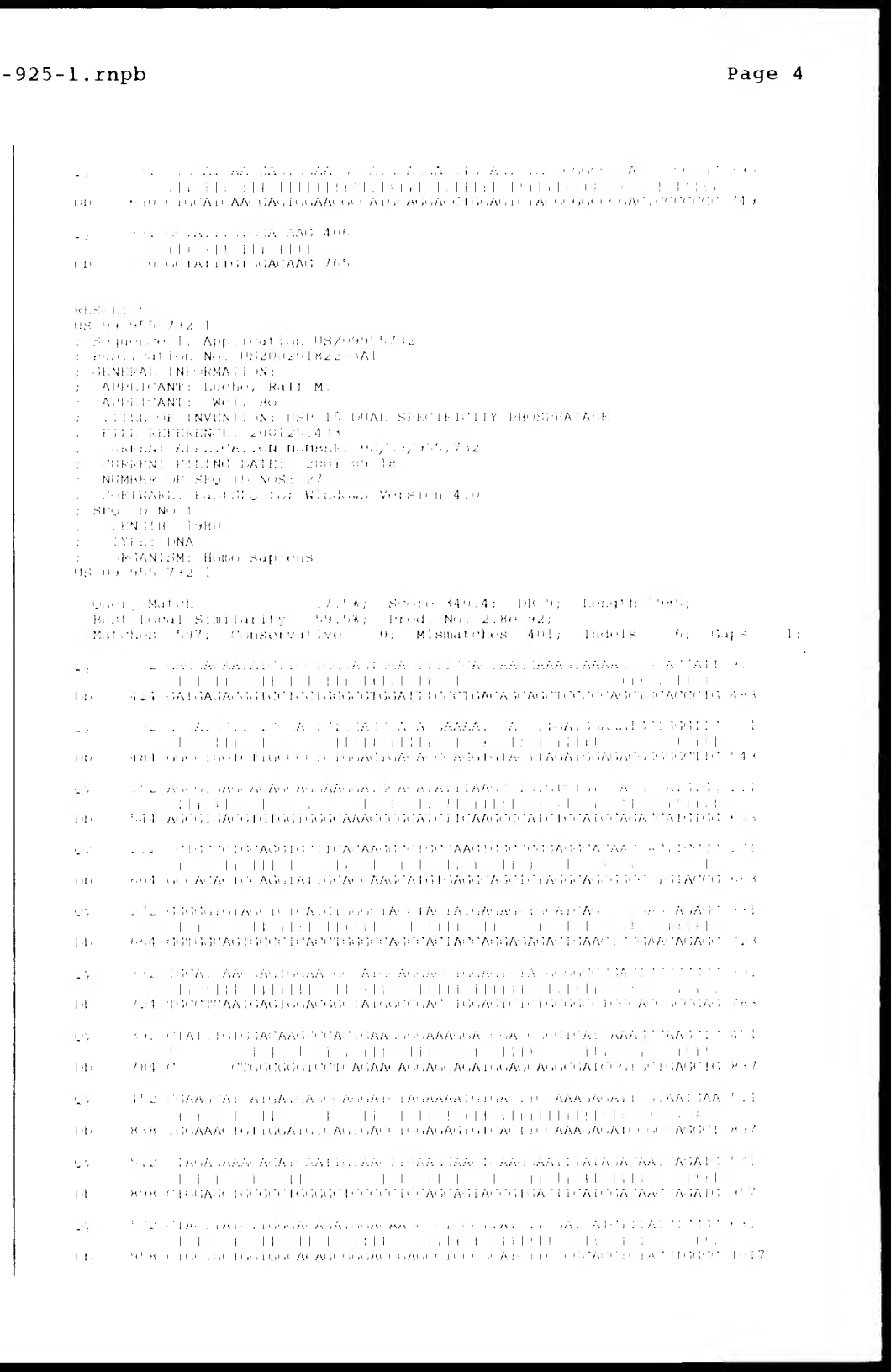

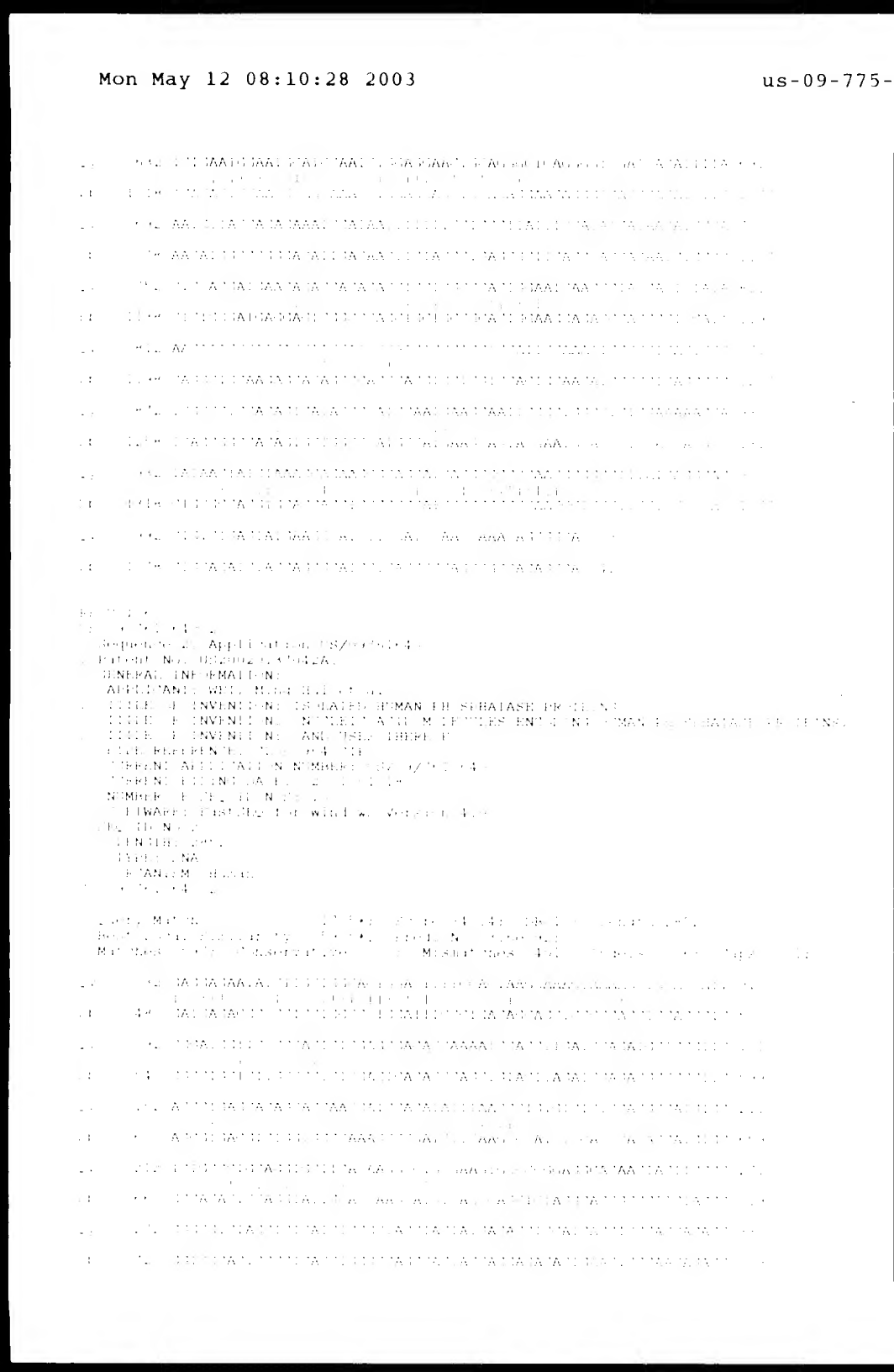

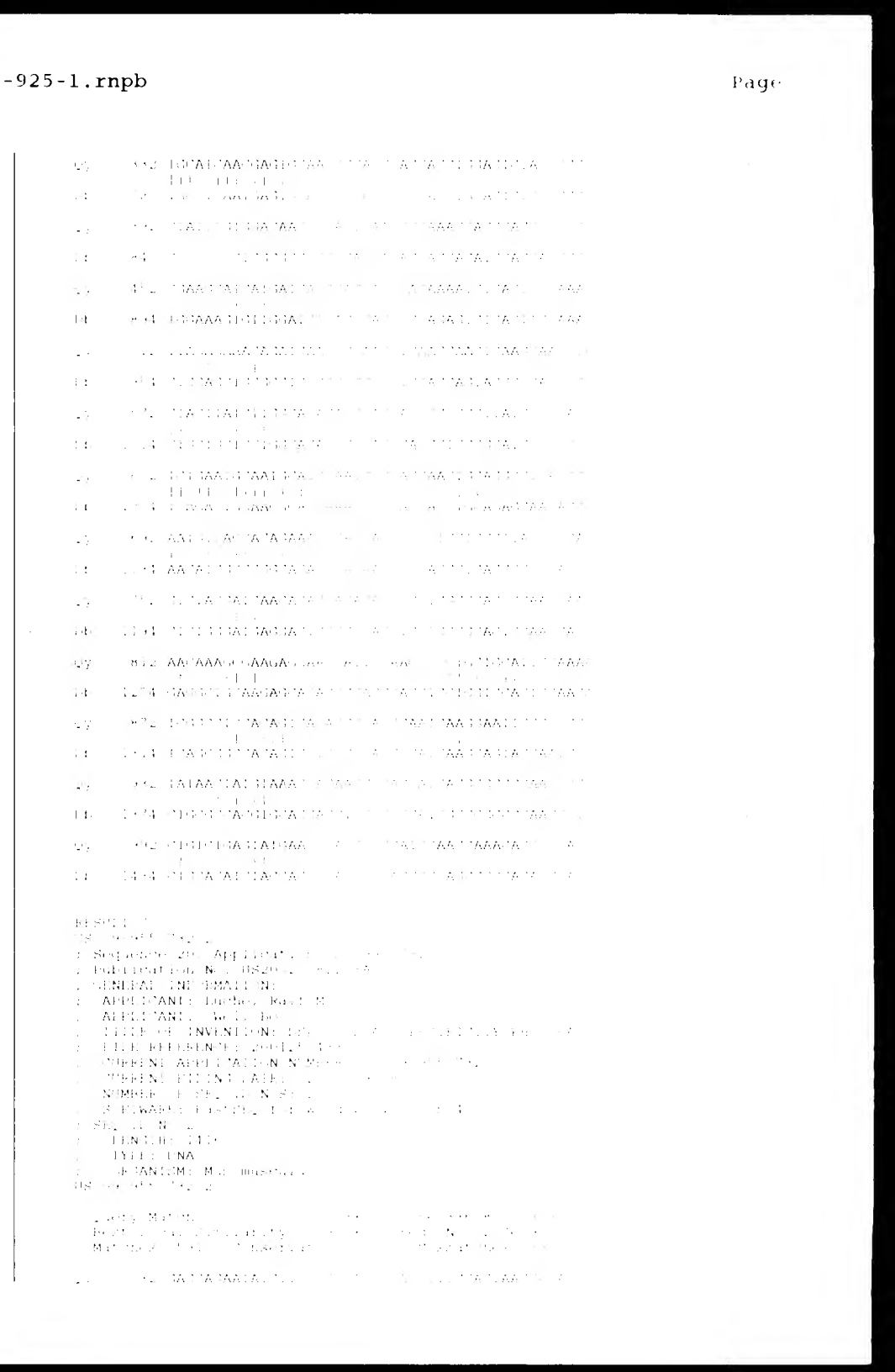

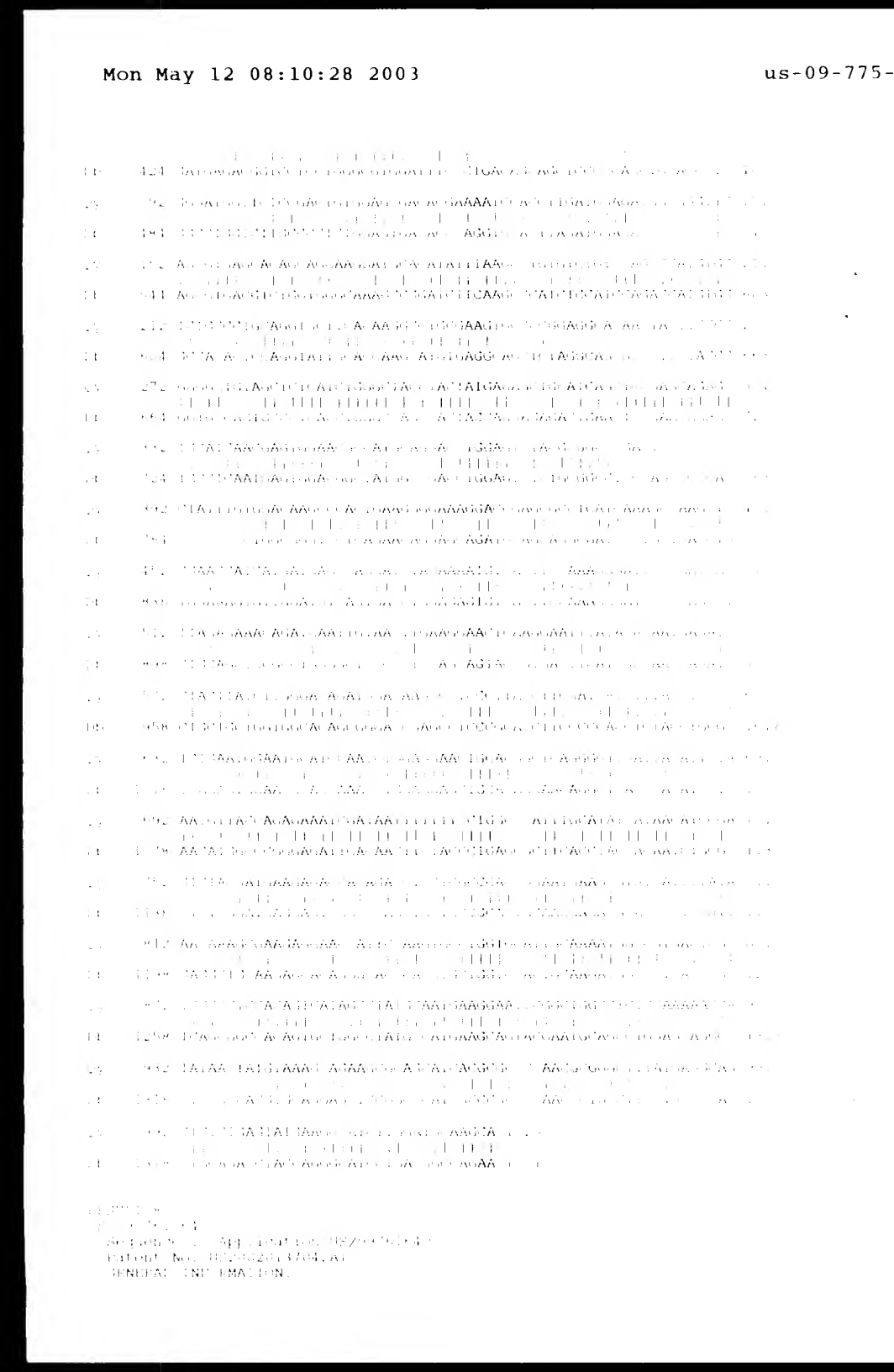

; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000964 CIP
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2704
; TYPE: DNA
; ORGANISM: Human

Query Match 17.4%; Score 346.8; DB 10; Length 2704;
Best Local Similarity 59.9%; Pred. No. 4.4e-91;
Matches 561; Conservative 0; Mismatches 397; Indels 6; Gaps 1;